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#2	Search rana pipiens AND ribonuclease	15:20:36	<u>35</u>
#1	Search rana pipiens	15:16:35	<u>5676</u>

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Jan 20 2004 07:12:30

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us-protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 25.7079 Seconds  
(without alignments)  
1043.940 Million cell updates/sec

Title: US-09-622-613C-2  
Perfect score: 578  
Sequence: 1 QDWLTFQKHLNTRDVCN.....TFCVTCENQAPVHVGVC 104

Scoring table: BL0SUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	127	13 Q918V8	Q918V8 rana pipien
2	556	96.2	127	13 Q8UYX5	Q8UYX5 rana pipien
3	404.5	70.0	129	13 Q8DFY6	Q8DFY6 rana pipien
4	386	66.8	128	13 Q8DFY8	Q8DFY8 rana pipien
5	311	53.8	128	13 Q8DFY7	Q8DFY7 rana pipien
6	309	53.5	128	13 Q8DFY5	Q8DFY5 rana pipien
7	298	51.6	133	13 Q8SMO	Q8SMO rana pipien
8	292	50.5	133	13 Q8SMO	Q8SMO rana pipien
9	286	49.5	133	13 Q8SMO	Q8SMO rana pipien
10	285	49.3	133	13 Q8SMO	Q8SMO rana pipien
11	282	48.8	133	13 Q8SMO	Q8SMO rana pipien
12	280	48.4	132	13 Q8SMO	Q8SMO rana pipien
13	275.5	47.7	132	13 Q8SMO	Q8SMO rana pipien
14	257.5	27.2	159	13 Q8W738	Q8W738 xenopus lae
15	129	22.3	152	11 Q9JK15	Q9JK15 mus saxicol
16	127	22.0	157	11 Q9JK19	Q9JK19 meriones un

17	126.5	21.9	153	11 Q9JK17	Q9JK17 mus saxicol
18	126	21.8	157	11 Q9JK3	Q9JK3 meriones un
19	125	21.6	157	11 Q9JK4	Q9JK4 meriones un
20	123	21.3	154	11 Q9JK8	Q9JK8 mus saxicol
21	122	21.1	157	11 Q9JK1	Q9JK1 meriones un
22	121	20.9	157	11 Q9JK2	Q9JK2 meriones un
23	120.5	20.8	155	11 Q9JK9	Q9JK9 mus pahari
24	119.5	20.7	155	11 Q9JK3	Q9JK3 mus saxicol
25	116.5	20.2	155	11 Q9JK6	Q9JK6 mus saxicol
26	115.5	20.0	132	6 Q9TV25	Q9TV25 eulemur ful
27	115.5	20.0	155	11 Q9JK12	Q9JK12 mus saxicol
28	115.5	20.0	155	11 Q9JK14	Q9JK14 mus saxicol
29	114.5	19.8	170	6 Q9BECL	Q9BECL tragulus ja
30	113.5	19.6	119	6 Q9TS06	Q9TS06 cercopithec
31	113.5	19.6	119	6 Q9TV32	Q9TV32 gorilla gor
32	113.5	19.6	132	6 Q9TV24	Q9TV24 galago mo
33	113.5	19.6	147	6 Q8H200	Q8H200 pan troglod
34	113.5	19.6	155	11 Q9R134	Q9R134 tatus norv
35	113	19.6	156	11 Q9JK6	Q9JK6 mus caroli
36	113	19.6	156	11 Q9JK7	Q9JK7 mus caroli
37	112.5	19.5	119	6 Q9TV30	Q9TV30 saginus oe
38	112.5	19.5	155	11 Q9R125	Q9R125 mus musculu
39	112.5	19.5	155	11 Q9JK8	Q9JK8 mus pahari
40	112	19.4	124	6 Q9TSF2	Q9TSF2 bos taurus
41	112	19.4	156	11 Q9JKG7	Q9JKG7 mus caroli
42	111.5	19.3	155	11 Q9JKG3	Q9JKG3 mus caroli
43	111	19.2	124	6 Q9SNE6	Q9SNE6 bubalus bub
44	111	19.2	156	6 Q8SQ04	Q8SQ04 lemur catra
45	111	19.2	156	11 Q9JKH4	Q9JKH4 mus caroli

## ALIGNMENTS

### RESULT 1

ID	Q918V8	PRELIMINARY	PRT	127 AA
AC	Q918V8			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Onconase variant rapRL precursor.			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxId=8404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	MEDLINE=2033057; PubMed=10871370;			
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V., Jr., Rybak S.M.;			
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a			
RT	3' UTR of unusual length and structure."			
RL	Nucleic Acids Res. 28:2375-2382(2000).			
DR	EMBL; AF165133; AAF76935.1; ..			
DR	HSSP; P22069; IONC.			
DR	InterPro; IPR001427; RNaseA.			
DR	Pfam; PF00074; RNaseA; 1.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.			
KW	SIGNAL.			
FT	SIGNAL			
FT	SEQUENCE			
FT	1 23			
FT	POTENTIAL.			
FT	SEQUENCE			
FT	127 AA; 14491 MW; B851DC5407AB69B CRC64;			

Query Match 100.0%; Score 578; DB 13; Length 127;

Best Local Similarity 100.0%; Pred. No. 4.3e-58;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 QDWLTFQKHLNTRDVCNIMSTNLFHCKDKNTFIYSRPPVRAICGIIASGNVLT 60
Db	24 QDWLTFQKHLNTRDVCNIMSTNLFHCKDKNTFIYSRPPVRAICGIIASGNVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 104  
DB 84 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 127

## RESULT 2

08UVX5 PRELIMINARY; PRT; 127 AA.

AC 08UVX5; PRELIMINARY; PRT; 127 AA.

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (T-EMBLrel. 23, Last annotation update)

DE Oncomase precursor.

GN RPR.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI\_TaxID=8404;

RN [1]

RP SEQUENCE FROM N.A.

RA Liao Y.-D., Wang S.-C.;

RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF321319; AAL54383.1; -

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase\_Pc; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

KM Signal.

FT SIGNAL.

SQ SEQUENCE 127 AA; 14469 MW; 953F90D31CEE3F CRC64;

Query Match 96.2%; Score 556; DB 13; Length 127;

Best Local Similarity 96.2%; Pred. No. 1.4e-55;

Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QDWLTFQKGLTNRDVDCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 60

DB 24 QDWLTFQKGLTNRDVDCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 104

DB 84 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 127

RESULT 3

09DFY6 PRELIMINARY; PRT; 129 AA.

AC 09DFY6; PRELIMINARY; PRT; 129 AA.

DT 01-MAR-2001 (T-EMBLrel. 16, Created)

DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)

DE RC-RNase4 ribonuclease precursor.

OS Rana catesbeiana (Bull. frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI\_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RT "Purification and cloning of cytoxic ribonucleases from Rana

catesbeiana (bullfrog)";

RT Nucleic Acids Res. 28:4097-4104 (2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

EMBL; AF242555; AAG31441.2; -

HS98; P22069; 10NC.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

KM Signal.

FT SIGNAL.

SQ SEQUENCE 129 AA; 14724 MW; 826A628B2B10ABDA CRC64;

Query Match 70.0%; Score 404.5; DB 13; Length 129;

Best Local Similarity 67.6%; Pred. No. 2.5e-38;

Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 1 QDWLTFQKGLTNRDVDCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 60

DB 24 QDWLTFQKGLTNRDVDCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 104

DB 84 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 128

RESULT 4

09DFY8 PRELIMINARY; PRT; 128 AA.

AC 09DFY8; PRELIMINARY; PRT; 128 AA.

DT 01-MAR-2001 (T-EMBLrel. 16, Created)

DT 01-MAR-2001 (T-EMBLrel. 18, Last sequence update)

DE RC-RNase2 ribonuclease precursor.

OS Rana catesbeiana (Bull. frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI\_TaxID=4400;

RN [1]

RP SEQUENCE FROM N.A.

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF242553; AAG31439.1; -

DR HSSP; P22069; 10NC.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

KM Signal.

FT SIGNAL.

SQ CHAIN 128 AA; 14839 MW; 989719CF52053CC CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;

Best Local Similarity 67.3%; Pred. No. 3.1e-36;

Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

OY 1 QDWLTFQKGLTNRDVDCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 60

DB 24 QDWLTFQKGLTNRDVDCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 104

DB 84 SEFYLSDCNVTSRPCKYKLTCKSTNTFCVTCENQAPVHFGVGHG 127

RESULT 5

09DFY7

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 11.6854 Seconds  
(without alignments)  
855.901 Million cell updates/sec

Title: US-09-622-613C-2  
Perfect score: 578  
Sequence: 1 ODMLTFQKHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	95.7	104	2 A39035	ribonuclease-relat
2	289	50.0	111	2 A27121	ribonuclease-relat
3	285.5	49.4	111	1 JX0120	ribonuclease-relat
4	269.5	46.6	111	2 JX0085	pancreatic ribonuc
5	149	25.8	119	2 S41111	pancreatic ribonuc
6	131	22.7	124	1 NRUI	pancreatic ribonuc
7	128	22.1	125	1 A32474	angiogenin [valida
8	126	21.8	128	1 NRCU	pancreatic ribonuc
9	125	21.6	124	1 NRMHK	pancreatic ribonuc
10	120	20.8	128	1 NRKS	pancreatic ribonuc
11	119.5	20.7	145	1 A35932	pancreatic ribonuc
12	119	20.6	128	1 NRCBP	angiogenin precurs
13	117	20.2	124	1 NRGP	pancreatic ribonuc
14	116	20.1	128	1 B43825	pancreatic ribonuc
15	116	20.1	128	1 NRYV	angiogenin - rabbi
16	114	19.7	124	1 NRHP	pancreatic ribonuc
17	113	19.6	127	1 NRHDUG	angiogenin precurs
18	112	19.4	124	1 NRBOB	pancreatic ribonuc
19	112	19.4	124	1 NRPG	pancreatic ribonuc
20	112	19.4	150	1 NRBO	pancreatic ribonuc
21	111.5	19.3	147	2 I52489	ribonuclease 4 (EC
22	111	19.2	124	2 S08549	ribonuclease - dom
23	111	19.2	128	1 NRHO	pancreatic ribonuc
24	111	19.2	128	1 NRPO	pancreatic ribonuc
25	110.5	19.1	127	2 S20066	pancreatic ribonuc
26	110.5	19.1	123	1 A43825	pancreatic-type ri
27	110.5	19.1	155	2 JC6159	angiogenin - pig
28	109	18.9	124	1 NRSH	eosinophil-associa
29	109	18.9	124	1 NRPH	pancreatic ribonuc

30	109	18.9	124	1 NRGA	pancreatic ribonuc
31	109	18.9	124	1 S07141	pancreatic ribonuc
32	108	18.7	124	1 NRMB	pancreatic ribonuc
33	108	18.7	124	1 NRGN	pancreatic ribonuc
34	107	18.5	124	1 NRNF	pancreatic ribonuc
35	106	18.3	156	2 JC6160	eosinophil-associa
36	105	18.2	124	1 NRDEO	pancreatic ribonuc
37	105	18.2	124	1 NRDM	pancreatic ribonuc
38	105	18.2	124	1 NRDM	pancreatic ribonuc
39	105	18.2	124	1 NRDM	pancreatic ribonuc
40	105	18.2	124	1 NRDM	pancreatic ribonuc
41	104	18.0	124	1 NRHY	pancreatic ribonuc
42	103	17.8	124	1 NRDER	pancreatic ribonuc
43	103	17.8	124	1 NRDN	pancreatic ribonuc
44	103	17.8	124	1 NRKN	pancreatic ribonuc
45	102	17.6	124	1 NRDEP	pancreatic ribonuc

## ALIGNMENTS

```
RESULT 1
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C/Species: Rana pipiens (northern leopard frog)
C/Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C/Accession: A39035
R/Ardele, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A/Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early
A/Reference number: A39035; MUID:91093131; PMID:1985896
A/Accession: A39035
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-104 <ARD>
C/Superfamily: pancreatic ribonuclease

Query Match      95.7%  Score 553, DB 2; Length 104;
Best Local Similarity 95.2%  Pred. No. 1.1e-48;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ODMLTFQKHLNTRDVCNINMSTNLFPHCKDKKTFIYSRPEPVKAICKGIASKNVLT 60
Db 1 EDMLTFQKHLNTRDVCNINMSTNLFPHCKDKKTFIYSRPEPVKAICKGIASKNVLT 60

Oy 61 SEFYLSDCNVTSPRCYKYLKKSSTNFCVTCENQAPVHFVGVGHC 104
Db 61 SEFYLSDCNVTSPRCYKYLKKSSTNFCVTCENQAPVHFVGVGSC 104

RESULT 2
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C/Accession: A27121
R/Titanium, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi,
Biochemistry 26, 2189-2194, 1987
A/Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A/Reference number: A27121; MUID:8729649; PMID:3304421
A/Molecule type: protein
A/Residues: 1-111 <RTT>
C/Superfamily: pancreatic ribonuclease
C/Keywords: lectin

Query Match      50.0%  Score 289, DB 2; Length 111;
Best Local Similarity 48.6%  Pred. No. 4.2e-22;
Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

Oy 1 ODMLTFQKHLNTRDVCNINMSTNLF---HCKDKKTFIYSRPEPVKAICKGIASKN 56
Db 1 ENWATFOQGHIIINTPIINCNTIMDNNIYIVGCGCKKVNPIIISATTVKALCTGVILNMN 59
```





R.Bond, M.D.; Strydom, D.J.  
Biochemistry 28, 6110-6113, 1989  
A:Title: Amino acid sequence of bovine angiotensin  
A:Reference number: A32474; MUID:89375344; PMID:2775757  
A:Accession: A32474  
A:Molecule type: protein  
A:Residues: 1-125 <BON>  
A:Experimental source: plasma  
R:Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.  
FEBS Lett. 241, 41-45, 1988  
A:Title: The complete amino acid sequence of bovine milk angiotensin.  
A:Reference number: S02001; MUID:89065101; PMID:3197838  
A:Accession: S02001  
A:Molecule type: protein  
A:Residues: 1-125 <MAE>  
A:Experimental source: milk  
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
submitted to the Brookhaven Protein Data Bank, January 1995  
A:Reference number: A65065; PDB:1AG1  
A:Contents: annotation: X-ray crystallography, 1.5 angstroms, residues 1-125  
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995  
A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.  
A:Reference number: A58315; MUID:95224057; PMID:7708754  
A:Contents: annotation: X-ray crystallography, 1.5 angstroms  
R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
submitted to the Brookhaven Protein Data Bank, April 1996  
A:Reference number: A65709; PDB:1G10  
A:Contents: annotation: conformation by (1)H-NMR, residues 1-125  
R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
Biochemistry 35, 8870-8880, 1996  
A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy.  
A:Reference number: A58821; MUID:96280645; PMID:8688423  
A:Contents: annotation: conformation by (1)H-NMR  
R:Reisdorf, C.; Abergl, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.  
Eur. J. Biochem. 224, 811-822, 1994  
A:Title: Proton resonance assignments and secondary structure of bovine angiotensin.  
A:Reference number: S48212; MUID:95010071; PMID:7925406  
A:Contents: annotation: conformation by (1)H-NMR  
A:Function:  
C:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation  
F:60-68/Region: receptor binding #status predicted  
F:14/41,115/Active site: His, Lys, His #status predicted  
F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 22.1%; Score 128; DB 1; Length 125;  
Best Local Similarity 34.0%; Pred. No. 7,66-06;  
Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

Oy 16 DVDGNNIMSTNLF--HCKDKNTFYRSREPVKAI CKGIISKN-----VLTTSFYL 65  
Db 24 DEYCFNNMKNNRLTRPCDKRTTFHGNKNDIKALICE-----DRNGQPYRGDIRISKSEFOI 79  
Oy 66 SDC---NWTSR-PCKYTKKSTNFTCVTCENQAVHF 98  
Db 80 TICRHKGGSSRPPCRGATGSDSRVIVGCENGLPVHF 116

RESULT 8  
NRCU pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
N:Alternate names: RNase 1; RNase A  
S:Species: Myocastor coypus (nutria, coypu)  
C:Date: 24-Apr-1994 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
C:Accession: A00822  
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
Biochim. Biophys. Acta 453, 400-409, 1976  
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
A:Reference number: A90612; MUID:77065676; PMID:999896  
A:Accession: A00822  
A:Molecule type: protein

A:Residues: 1-128 <VAN>  
C:Superfamily: pancreatic ribonuclease  
K:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.8%; Score 126; DB 1; Length 128;  
Best Local Similarity 29.9%; Pred. No. 1,2e-05;  
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

OY 6 FOKKL-----TNTRDVDCNIM-STLNF--HCKDKPTFYSPBPVKAICKGIASKNV 57  
|::||:| |::||:| |::||:| |::||:| |:  
DB 8 PERQMDNSGSGSTNNYNNEEMAKSRMTGRCRKPVTTFPEPLADVAVC----FOKNV 63  
|::||:| |::||:| |::||:| |::||:| |:  
OY 58 L-----TTSEFYLSDCNVTSRP---CKYLKKSTNTFCVTCENO--APVHF 98  
|::||:| |::||:| |::||:| |::||:| |:  
DB 64 LCKNGQTNCYQSNMNHITDCRVTSNSDYPNCISYRTSQEKSIVAVACEGNPVVPVHF 120  
|::||:| |::||:| |::||:| |::||:| |:

RESULT 9  
NRMK  
pancreatic ribonuclease (BC 3.1.27.5) - minke whale  
N:Alternate names: RNase A  
C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)  
C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C:Accession: A00818  
R:Eimers, M.; Welling, G.W.; Beintema, J.J.  
Biochem. J. 157, 317-323, 1976  
A>Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.  
A:Reference number: A00818; MUID:76277855; PMID:962870  
A:Accession: A00818  
A:Molecule type: protein  
A:Residues: 1-124 <EMW>  
C:Superfamily: pancreatic ribonuclease  
K:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.6%; Score 125; DB 1; Length 124;  
Best Local Similarity 28.6%; Pred. No. 1,5e-05;  
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 4 LTFQKHLLTNTRDVD-----CNINISTNLF---HCKDKPTFYSPBPVKAICKGIASK 55  
|::||:| |::||:| |::||:| |::||:| |:  
DB 6 MKFORQHDSGNSPGNNPNPCNMRRKRKTGCRCRPVTFVHESLEDAVAC---SOK 61  
|::||:| |::||:| |::||:| |::||:| |:  
OY 56 NVL-----TTSEFYLSDCNVTSRP---CKYLKKSTNTFCVTCENO--APVHF 98  
|::||:| |::||:| |::||:| |::||:| |:  
DB 62 NVLCKNGRTCYENSTNHTIDCRGTGSSSKPYCAVKTSQEKHIIVACEGNPVVPVHF 120  
|::||:| |::||:| |::||:| |::||:| |:

RESULT 10  
NRKS  
pancreatic ribonuclease (EC 3.1.27.5) - castragua  
C:Species: Proechimys guairae (castragua)  
C>Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 30-Sep-1993  
C:Accession: A00821  
R:Beintema, J.J.; Knol, G.; Matrena, B.  
Biochim. Biophys. Acta 705, 102-110, 1982  
A>Title: The primary structures of pancreatic ribonucleases from African porcine and c  
A:Reference number: A90644; MUID:83000399; PMID:7115727  
A:Accession: A00821  
A:Molecule type: protein  
A:Residues: 1-128 <BRI>  
A>Note: residues 67-78 were positioned primarily by homology with other ribonucleases  
C:Superfamily: pancreatic ribonuclease  
K:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 (without alignment) 784.758 Million cell updates/sec

Title: US-09-622-613C-2  
Perfect score: 578  
Sequence: 1 QDWLTFQKHLTNRDVDCN.....TFCVTCENQAPHFVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	96.2	104	1	RN30_RANPI
2	292	50.5	111	1	RNPO_RANCA
3	285.5	49.4	111	1	LECS_RANCA
4	269.5	46.6	111	1	RNPL_RANCA
5	149	25.8	119	1	RNP_IGUG
6	131	22.7	124	1	RNP_GALMU
7	130.5	22.6	145	1	ANGR_MOUSE
8	130.5	22.6	146	1	ANGI_CERAE
9	128	22.1	148	1	ANGI_BOVIN
10	126	21.8	128	1	RNP_MYOCO
11	125	21.6	124	1	RNP_BALAC
12	121.5	21.0	146	1	ANGI_MACMU
13	120	20.7	128	1	RNP_BROCU
14	119.5	20.7	145	1	ANGI_MOUSE
15	119	20.6	128	1	RNBP_CAVPO
16	118.5	20.5	146	1	ANGI_PAPHA
17	117	20.2	124	1	RNP_CHIRR
18	116	20.1	125	1	ANGI_RABIT
19	116	20.1	128	1	RNP_HYDRI
20	114	19.7	124	1	RNP_HIPAM
21	114	19.7	146	1	ANGI_MIOTA
22	113	19.6	147	1	ANGI_HUMAN
23	113	19.6	147	1	ANGI_PANTR
24	112	19.4	124	1	RNP_PIG
25	112	19.4	150	1	RNP_BOVIN
26	112	19.3	156	1	RNP_MYOCU
27	111.5	19.3	147	1	RNS4_HUMAN
28	111	19.2	128	1	RNP_HORSE
29	111	19.2	156	1	RNP_HYSCR
30	111	19.2	167	1	RNBR_BOVIN
31	111	19.2	123	1	ANGI_PIG
32	110.5	19.1	133	1	ECPI_MOUSE
33	110.5	19.1	155	1	ECPI_MOUSE

## ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	104 AA.
RN30_RANPI					
AC	P22069	01-AUG-1991 (Rel. 19, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OS	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.				
OX	NCBI_TaxID=8404;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Embryo;				
RX	MEDLINE=91053131; Pubmed=1985896;				
RA	Ardelt W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens				
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=93066156; Pubmed=1438177;				
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;				
RT	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein:				
RT	a novel antitumor protein of Rana pipiens oocytes and early				
RL	embryos.";				
RN	Proteins 14:392-400(1992).				
RP	[3]				
RX	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RA	Mosimann S.C., Ardelt W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an				
RT	amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY				
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR				
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH				
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: P00074; RNaseA.				
DR	ProDom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase_Pc; 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure;				
KW	Pyroliidone carboxylic acid.				
FT	MOD_RES	1			
FT	ACT_SITE	10			
FT	ACT_SITE	31			
FT	ACT_SITE	97			
FT	DISULFID	19			
FT	DISULFID	30			
FT	DISULFID	75			

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FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

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Query Match 96.2%; Score 556; DB 1; Length 104;  
 Best Local Similarity 96.2%; Pred. No. 1,6e-52;  
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 ODMLTQKHLNTRDVDCNNIMSTNLFPHCKDNTFIYSRPEPVKAICKGIISKVLT 60
Db 1 ODMLTQKHLNTRDVDCNNIMSTNLFPHCKDNTFIYSRPEPVKAICKGIISKVLT 60
Oy 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
Db 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104

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## RESULT 2

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ID RNPO_RANCA STANDARD; PRT; 111 AA.
AC P11916;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RA "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [2]
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RA "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [3]
RP CHARACTERIZATION.
RC TISUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RA "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [4]
RP STRUCTURE BY NMR.
RN [1]

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RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RA "The solution structure of a cytototoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
CC as substrates, and prefers the former. The 5-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A27121; A27121.
DR PDB; 1BC4; 28-OCT-98.
DR PDB; 1M07; 21-JAN-03.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
FT DISULFID 93 110
FT HELIX 3 10
FT HELIX 19 23
FT TURN 26 27
FT TURN 37 41
FT STRAND 45 51
FT TURN 52 52
FT STRAND 57 62
FT STRAND 68 73
FT STRAND 83 88
FT STRAND 92 97
FT TURN 98 99
FT STRAND 100 107
SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;
Query Match 50.5%; Score 292; DB 1; Length 111;
Best Local Similarity 49.5%; Pred. No. 2.1e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;
Oy 1 ODMLTQKHLNTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIISKV 56
Db 1 ODMLTQKHLNTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIISKV 56
Oy 57 VLTTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
Db 60 VLSTFRQALNCTKRTSITPRPCYSRTETNIVCVGCENQAPVHFGVGHG 110

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RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RA MEDLINE=91035319; PubMed=2229005;
RA Kamuya Y., Oyama F., Sakakibara F., Nitta K., Kawachi H.,
RA Takayanagi Y., Tlanti K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR: JX0120; JX0120.
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyroliadone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT Eukaryotic 34 82
FT DISULFID 52 97
FT DISULFID 94 111
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 49.4%; Score 285.5; DB 1; Length 111;
Best Local Similarity 45.0%; Pred. No. 1e-23;
Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFTYSRPEPVKAIKGIASKN 56
DB 1 QNMAKFKKXIRSTSIDCNTIMDKAIYIVGCKCKERTFTIISSEDNVKAICSGVSPRK 60
QY 57 VLTSEFYLSDC---NTSRPCKYKLLKSTNFTCYTCENQAPVHFGVGHG 104
DB 61 VLSSTFPLNLCIRSATAPRCPYNSRSTETNVIQVCKENRLLPVHFGIGRC 111

RESULT 4
RNP_LIGUG STANDARD; PRT; 111 AA.
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
liver."
RL J. Biochem. 106:729-735(1989).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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DR PIR: JX0085; JX0085.
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Pyroliadone carboxylic acid.
KW Pyroliadone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 46.6%; Score 269.5; DB 1; Length 111;
Best Local Similarity 43.2%; Pred. No. 5.2e-22;
Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFTYSRPEPVKAIKGIASKN 56
DB 1 QNMAKFKKXIRSTSIDCNTIMDKAIYIVGCKCKERTFTIISSEDNVKAICSGVSPRK 60
QY 57 VLTSEFYLSDC---NTSRPCKYKLLKSTNFTCYTCENQAPVHFGVGHG 104
DB 61 ELSTTFPLNLCIRSATAPRCPYNSRSTETNVIQVCKENRLLPVHFGIGRC 111

RESULT 5
RNP_LIGUG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RA MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
ribonuclease."
RL Eur. J. Biochem. 219:641-646(1994).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR: S4111; S4111.
DR HSSP: P00656; 1LSQ.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Pyroliadone carboxylic acid.
KW Pyroliadone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT DISULFID 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.

```

SO SEQUENCE 119 AA; 13324 MW; 6072F85B7B15BD5A CRC64;

Query Match 25.8%; Score 149; DB 1; Length 119;  
Best Local Similarity 30.7%; Pred. No. 3.7e-09;  
Matches 35; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

QY 1 QWLTFRQKHL-----TTRVDVCCNNIM--STNLFCKDKKTFYISRPPEVKAIC--K 49  
DB 1 QWMSFQNHIDYIPETSASNPAYCDLMQORNLNPTKTRNTFVHASPSEIQOVCSGS 60  
QY 50 GIASKNVLTTSF-FYLSDC---NVTSPCKYKLKSTNFCVTCENQAPVHF 98  
DB 61 GTHYEDNLDSNESFBLDCKNVGCTAPSSCKTNGTPIKRIAIACENQPVHF 114

## RESULT 6

RNP\_GALMU STANDARD; PRT; 124 AA.

AC P00680; 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
GN Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
OS RNASL OR RNSI.  
OC Galea musteloides (Cuiis).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Galea.  
OX NCBI\_TaxId=10146;  
RN (1) \_SEQUENCE.  
RX MEDLINE=87036770; PubMed=6571219;  
RA Beintema J.J., Neuteboom B.;  
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives: capybara and cuiis ribonuclease.";  
RT J. Mol. Evol. 19:145-152(1983).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Pancreas.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR PIR: A00827; NRU1.  
DR HSSP: P00656; ISRN.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaaseA.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR ProDom: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR ProSITE: PS00127; RNASE\_PANCREATIC.1.  
KM Hydrolyase; Nuclease; Endonuclease.  
FT DISULFID 26 84 BY SIMILARITY.  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 65 72 BY SIMILARITY.  
FT ACT\_SITE 12 12 BY SIMILARITY.  
FT ACT\_SITE 41 41 BY SIMILARITY.  
FT ACT\_SITE 119 119 BY SIMILARITY.  
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).  
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.7%; Score 131; DB 1; Length 124;  
Best Local Similarity 30.6%; Pred. No. 3.2e-07;  
Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

QY 4 LTFQKHL-----TTRVDVCCNNIM--STNLFCKDKKTFYISRPPEVKAICGGIA 53  
DB 6 MKFORQHMDSGDHPDNTN--YCNEMVVRSMTOGCKPVTFFVHEPLEAVQAVC---S 59  
QY 54 SKNV-----LTTSEFYSDCNVTSR---CKYKLKSTNFCVTCEN--QAPVH 97  
DB 60 QKAVPCKNGCTNCYQSHSMRTIDCRVTSSSKYPNCSTYRMTQAKSIIVACGTPSVVPH 119

QY 98 F 98  
DB 120 F 120

## RESULT 7

ANGR\_MOUSE STANDARD; PRT; 145 AA.

AC 064438; 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
GN Angiogenin-related protein precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN (1) \_SEQUENCE FROM N.A.  
RP STRAIN=129; TISSUE=Liver;  
RX MEDLINE=96079109; PubMed=8530072;  
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;  
RT "The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes";  
RT Genomics 29:200-206(1995).  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
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DR EMBL: U2519; AAA91367.1; -  
DR HSSP: P03950; 1A4Y.  
DR MOD: MGI:104984; AngRP.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaaseA.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR ProDom: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR ProSITE: PS00127; RNASE\_PANCREATIC.1.  
KM Signal; Hydrolyase; Nuclease; Endonuclease;  
FT SIGNAL 1 24 PYROLIDONE CARBOXYLIC ACID.  
FT CHAIN 25 145 POTENTIAL.  
FT MOD\_RES 25 145 ANGIOGENIN-RELATED PROTEIN.  
FT ACT\_SITE 37 37 PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 137 137 BY SIMILARITY.  
FT DISULFID 50 104 BY SIMILARITY.  
FT DISULFID 63 115 BY SIMILARITY.  
FT DISULFID 81 130 BY SIMILARITY.  
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C9AD CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 145;  
Best Local Similarity 38.2%; Pred. No. 4.3e-07;  
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 30 CVDKNTFYISRPPEVKAIC--KGIIASKV-LTTSEFYSDCNVTSR---PCKYKLKKS 82  
DB 63 CVDVTFHIDTKNNIAVIGCKGSPYGRNLRIKSKRFQYTTCTHKGSRPRPCRYASKG 122  
QY 83 TMTFCVTCENQAPVHF 98  
DB 123 FRTIITGCGNVPVHF 138

## RESULT 8



ANGI\_CERAE STANDARD; PRT; 146 AA.

AC O8WN66;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNAse 5).  
 GN ANG OR RNASE5.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 NC NCB1\_TaxID=9534;  
 RN NCB1  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21918422; PubMed=11919285;  
 RA Zhang J., Rosenberg H.F.;  
 RT "Divergiting selection of the tumor-growth promoter angiogenin in  
 RT primate evolution.";  
 RL Mol. Biol. Evol. 19:438-445(2002).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC  
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 CC  
 CC  
 CC EMBL; AF41664; AAL61646.1; .  
 DR InterPro; IPR001427; RNAseA.  
 DR Pfam; PF00074; RNAseA; 1.  
 DR ProDom; PD000535; RNAseA; 1.  
 DR SMART; SM00092; RNAse\_Pc; 1.  
 DR PROSITE; PS00127; RNAse\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KM Protein synthesis inhibitor; Signal; Pyrolydione carboxylic acid.  
 FT SIGNAL 1 24  
 FT CHAIN 25 146  
 FT MOD\_RES 25 25  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64  
 FT ACT\_SITE 138 138  
 FT DISULFID 50 105  
 FT DISULFID 63 116  
 FT DISULFID 81 131  
 FT DISULFID 131 131  
 SQ SEQUENCE 146 AA; 16444 MW; 27860112858BD99 CRC64;  
 Query Match 22.6%; Score 130.5; DB 1; Length 146;  
 Best Local Similarity 30.7%; Pred. No. 4,4e-07;  
 Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;  
 QY 5 TFOKGLINTRDVDCNNIMSTNLHCKDKDTFYISREPVKAIG--KGIYASKNV-LTT 60  
 DB 53 TMRRRHITSP-----CKDINTFIHGNRHIIKATIGDNGNPYGNLISK 97  
 QY 61 SEFYLSDCNVT---RCKYKLLKSTNTPCVTGENDAPYH 97  
 DB 98 SPFOVTTCNLRGSGPRPPCOTRATRGSRNIVYGCENGLPVH 138  
 RESULT 9  
 ANGI\_BOVIN

ID ANGI\_BOVIN STANDARD; PRT; 148 AA.

AC P10152; O9GK9;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin-1 precursor (EC 3.1.27.-).  
 GN ANGI OR ANG.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NC NCB1\_TaxID=9913;  
 RN NCB1  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Chang S.-I.;  
 RT "Cloning, sequencing, and expression of bovine angiogenin.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN  
 RN SEQUENCE OF 24-148.  
 RP TISSUE=Milk;  
 RX MEDLINE=89065101; PubMed=3197838;  
 RA Maae P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;  
 RT "The complete amino acid sequence of bovine milk angiogenin.";  
 RL FEBS Lett. 241:41-45(1988).  
 RN  
 RN SEQUENCE OF 24-148.  
 RP TISSUE=Plasma;  
 RX MEDLINE=89375344; PubMed=2775757;  
 RA Bond M.D.; Strydom D.U.;  
 RT "Amino acid sequence of bovine angiogenin.";  
 RL Biochemistry 28:6110-6113(1989).  
 RN  
 RN CHARACTERIZATION, AND SEQUENCE OF 25-55.  
 RP TISSUE=Plasma;  
 RX MEDLINE=89118214; PubMed=3064806;  
 RA Bond M.D.; Vallee B.L.;  
 RT "Isolation of bovine angiogenin using a placental ribonuclease  
 RT inhibitor binding assay.";  
 RL Biochemistry 27:6282-6287(1988).  
 RN  
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RP MEDLINE=95224057; PubMed=7708754;  
 RA Acharya K.R., Shapiro R., RJordan R., Vallee B.L.;  
 RT "C-terminal structure of bovine angiogenin at 1.5-A resolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).  
 RN  
 RN STRUCTURE BY NMR.  
 RP MEDLINE=96280645; PubMed=8688423;  
 RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;  
 RT "Solution structure of bovine angiogenin by 1H nuclear magnetic  
 RT resonance spectroscopy.";  
 RL Biochemistry 35:8870-8880(1996).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL  
 CC RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC  
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 CC



Db 6 MKFORHNDGNSPGNNPNYCNQMMRRKMTGRCCKPVTFTVHESLEDKAVC-----SQK 61  
 QY 56 NVL-----TSEFYLSDCNVTSRP-----CKYKXKKSNTFTCVTCENQ--APVHF 98  
 Db 62 NVLCXNGRTNCTYESNTHWITDCROTGGSSKYPNCAYKTSQEKHIIIVACEGNPVYVHF 120

## RESULT 12

ANGI\_MACMU STANDARD; PRT; 146 AA.

AC Q8W63; 2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnaase 5).  
 GN ANG OR RNASE5.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21918422; PubMed=11919285;  
 RA Zhang J., Rosenberg H.F.;  
 RT "Diversifying selection of the tumor-growth promoter angiogenin in  
 RL primate evolution.";  
 RL Mol. Biol. Evol. 19:438-445 (2002).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC -----  
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 CC -----  
 DR EMBL: AF41667; AAL61649.1;  
 DR InterPro: IPR001427; Rnaase.  
 DR Pfam: PF00074; RnaaseA; 1.  
 DR ProDom: PD000535; RnaaseA; 1.  
 DR SMART: SM00092; Rnaase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KM Protein synthesis inhibitor; Signal; Pyrolydione carboxylic acid.  
 FT SIGNAL 1 24  
 FT CHAIN 25 146  
 FT MOD\_RSS 25 25  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64  
 FT ACT\_SITE 138 138  
 FT DISULFID 50 105  
 FT DISULFID 63 116  
 FT DISULFID 81 131  
 SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;

Query Match 21.0%; Score 121.5; DB 1; Length 146;  
 Best Local Similarity 28.7%; Pred. No. 4e-06;  
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

QY 5 TFOKHLTNTRDVDCNNIMSTNLFHCKDKNTFTYSRREPVAIC--KGIASKNV-LTT 60  
 Db 53 TMRRLHTSP-----CKDINTFVGNRHHTAITACGDEGSPYGNLRIST 97

QY 61 SEFYLSDCNVTS-----RCKYKXKKSNTFTCVTCENQAPVH 97  
 Db 98 SPFOVTTCKLRGSGPRPCQYRATRGSRNIVVGCENGLPVH 138

## RESULT 13

RNP\_PROGU STANDARD; PRT; 128 AA.

AC P04059;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnaase 1) (Rnaase A).  
 GN RNASE1 OR RN1.  
 OS Proechimys guairae (Caiaaguana).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Echimyidae; Proechimyys.  
 OX NCBI\_TaxID=10163;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=83000399; PubMed=7115727;  
 RA Beintema J.J., Knol G., Martena B.;  
 RT "The primary structures of pancreatic ribonucleases from African  
 RL porcupine and castor, two hystricomorph rodent species.";  
 RL Biochim. Biophys. Acta 705:102-110 (1982).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Pancreas.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PIN: A00821; NRKS.  
 DR HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; Rnaase.  
 DR Pfam: PF00074; RnaaseA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RnaaseA; 1.  
 DR SMART: SM00092; Rnaase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84  
 FT DISULFID 40 95  
 FT DISULFID 58 110  
 FT DISULFID 65 112  
 FT ACT\_SITE 12 12  
 FT ACT\_SITE 41 41  
 FT ACT\_SITE 119 119  
 FT CARBOHYD 34 34  
 SEQUENCE 128 AA; 14244 MW; 2DB58093A9D0C936 CRC64;

Query Match 20.8%; Score 120; DB 1; Length 128;  
 Best Local Similarity 29.9%; Pred. No. 4.9e-06;  
 Matches 35; Conservative 19; Mismatches 36; Indels 28; Gaps 7;

QY 6 FOKHLL-----TNTRDVDCNNIM-STNLF--HCKDKNTFTYSRREPVAICKGIASKNV 57  
 Db 8 FOROHIDSGSPSTNPYCNAMKMSRMTOERCKPVTFTVHEPLADYQAVC-----FOKNV 63  
 QY 58 -----LTTSEFYLSDCNVTSR-----PCKYKXKKSNTFTCVTCENQ--APVHF 98  
 Db 64 PCKXGNSCTYESNTHWITDCRLTNSKSPDCLYRISQEKSIIVACEGNPVYVHF 120

## RESULT 14

ANGI\_MOUSE STANDARD; PRT; 145 AA.  
 ID ANGI\_MOUSE  
 AC P21570;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnaase 5).

```

GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995 (1990).
RN [2]
RP PARTIAL SEQUENCE.
RX TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186 (1993).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
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CC
CC EMBL: U22516; AAA91366.1; -.
CC DR PIR: A35932; A35932.
CC DR HSSP: P03950; 1A4Y.
CC DR MGD: MGI:88022; Ang.
CC DR InterPro: IPR001427; RNaseA.
CC DR pfam: PF00074; RNaseA.1.
CC DR PRINTS: PR00794; RIBONUCLEASE.
CC DR ProDom: PD000535; RNaseA.1.
CC DR SMART: SM00092; RNase_Pc.1.
CC DR PROSITE: PS00127; RNASE_PANCREATIC.1.
CC KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
CC Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
CC FT SIGNAL 1 24
CC FT CHAIN 25 145
CC FT MOD_RES 25 25
CC FT ACT_SITE 37 37
CC FT ACT_SITE 64 64
CC FT ACT_SITE 137 137
CC FT DISULFID 50 104
CC FT DISULFID 63 115
CC FT DISULFID 81 130
CC SQ SEQUENCE 145 AA; 16228 MW; 06944260B8764938 CRC64;
Query Match 20.7%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 6.4e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;
QY 9 KHLTNRDNDV-----CNINSTNLF--HCKDKNTFIYSRPEPVKALC--KGIIASKN 56
DB 32 KFLTQHHDAKPKGRDRDYKCRMMKRSRLTSPCKDVNTFIIHGKSNKAIKICANGANGSPYREN 91
QY 57 V-LITSEFYISDCNVTN-----RPCKYKLKSKSTNTFCVTGQAPVHF 98
DB 92 LRMSKSPFOVTTCKHTGSGPRPCQYRASAGFRHVIVACENGPLVHF 138

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RESULT 15
RNPB_CAVPO STANDARD; PRT; 128 AA.
ID RNPB_CAVPO
AC P00679;
DT 21-UTL-1986 (Rel. 01, Created)
DT 21-UTL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease Pancreatic B (EC 3.1.27.5) (RNase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OK NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX TISSUE=Pancreas;
RX MEDLINE=77185023; PubMed=862624;
RA van den Berg A., van den Herde-Timmer L., Hofsteenge J., Gaastera W.,
RA Beintema J.J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation.";
RL Eur. J. Biochem. 75:91-100 (1977).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC DR HSSP: P00656; 1SRN.
CC DR InterPro: IPR001427; RNaseA.
CC DR pfam: PF00074; RNaseA.1.
CC DR PRINTS: PR00794; RIBONUCLEASE.
CC DR ProDom: PD000535; RNaseA.1.
CC DR SMART: SM00092; RNase_Pc.1.
CC DR PROSITE: PS00127; RNASE_PANCREATIC.1.
CC KM Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
CC FT DISULFID 26 84
CC FT DISULFID 40 95
CC FT DISULFID 58 110
CC FT DISULFID 65 72
CC FT ACT_SITE 12 12
CC FT ACT_SITE 41 41
CC FT ACT_SITE 119 119
CC FT CARBOHYD 21 21
CC FT CARBOHYD 34 34
CC FT VARIANT 64 64 L -> P.
CC SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E938 CRC64;
Query Match 20.6%; Score 119; DB 1; Length 128;
Best Local Similarity 28.3%; Pred. No. 6.3e-06;
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;
QY 4 LTFQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPVKALCKGIIAS 54
DB 6 MKFQRMHMBEGSPSSSNV--CVMVMIRRMNTGGRCKPNTFVHESLADVQAVC----FQ 60
QY 55 KNLV-----TTFEFLSDCNVTNRP-----CKYKLKSKSTNTFCVTGQAPVHF 98
DB 61 KNLVCKNGQGTNCVQGSRRRITDCRVTSSSKFPCNGCYRMSQAQSIIVACEGDPYVHF 120

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Search completed: January 22, 2004, 12:02:08  
Job time: 7.2321 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 Search time 24.7341 Seconds  
(without alignments)

869.271 Million cell updates/sec

Title: US-09-622-613C-2

578

Perfect score: 1 QDWLTFQKXHLTNRDVDCN.....TFCVTCENQAPVHFGVGHG 104

Sequence: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scoring table: 777136 seqs, 20673638 residues

Searched: 777136 seqs, 20673638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578	100.0	104	11	US-09-961-400-2
2	578	100.0	105	11	US-09-948-391A-6
3	578	100.0	105	11	US-09-961-400-6
4	578	100.0	127	11	US-09-948-391A-28
5	578	100.0	127	11	US-09-961-400-28
6	575	99.5	111	11	US-09-961-400-9
7	573	99.1	104	11	US-09-948-391A-11
8	573	99.1	104	11	US-09-961-400-11
9	573	99.1	105	11	US-09-948-391A-13
10	573	99.1	105	11	US-09-961-400-13
11	569	98.4	104	11	US-09-948-391A-2
12	569	98.4	104	11	US-09-948-391A-4
13	569	98.4	104	11	US-09-961-400-4
14	565	97.8	105	11	US-09-961-400-8
15	560	96.9	105	11	US-09-948-391A-8

16	560	96.9	111	11	US-09-948-391A-9	Sequence 9, Appl1
17	556	96.2	105	15	US-10-153-882-2	Sequence 2, Appl1
18	551	95.3	104	10	US-09-986-119-1	Sequence 1, Appl1
19	551	95.3	104	11	US-09-918-887-1	Sequence 3, Appl1
20	445	77.0	83	10	US-09-986-119-3	Sequence 15, Appl1
21	445	77.0	83	11	US-09-918-887-3	Sequence 3, Appl1
22	281.5	48.7	110	11	US-09-948-391A-15	Sequence 15, Appl1
23	281.5	48.7	110	11	US-09-961-400-15	Sequence 15, Appl1
24	281.5	48.7	111	11	US-09-961-400-17	Sequence 17, Appl1
25	277.5	48.0	110	11	US-09-961-400-19	Sequence 19, Appl1
26	277.5	48.0	111	11	US-09-948-391A-21	Sequence 21, Appl1
27	277.5	48.0	111	11	US-09-961-400-21	Sequence 21, Appl1
28	277.5	48.0	117	11	US-09-948-391A-22	Sequence 22, Appl1
29	277.5	48.0	117	11	US-09-961-400-22	Sequence 22, Appl1
30	276.5	47.8	110	11	US-09-948-391A-24	Sequence 24, Appl1
31	276.5	47.8	110	11	US-09-961-400-24	Sequence 24, Appl1
32	276.5	47.8	111	11	US-09-948-391A-26	Sequence 26, Appl1
33	276.5	47.8	111	11	US-09-961-400-26	Sequence 26, Appl1
34	275.5	47.7	111	11	US-09-948-391A-17	Sequence 17, Appl1
35	271.5	47.0	110	11	US-09-948-391A-19	Sequence 19, Appl1
36	157.5	27.2	169	13	US-10-016-447-2	Sequence 2, Appl1
37	149	25.8	119	12	US-10-074-978A-139	Sequence 139, App
38	128.5	22.2	124	13	US-10-016-447-5	Sequence 5, Appl1
39	113	19.6	147	9	US-09-286-240-6	Sequence 6, Appl1
40	113	19.6	147	9	US-09-863-777-2	Sequence 2, Appl1
41	113	19.6	147	10	US-09-731-872-254	Sequence 254, App
42	113	19.6	147	12	US-09-876-997-254	Sequence 254, App
43	112	19.4	124	10	US-09-981-286A-8	Sequence 8, Appl1
44	106.5	18.4	99	12	US-10-074-978A-141	Sequence 141, App
45	104.5	18.1	89	12	US-10-074-978A-143	Sequence 143, App

#### ALIGNMENTS

RESULT 1  
US-09-961-400-2  
Sequence 2, Application US/09961400  
Publication No. US2003012131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-961-400-2

Query Match 100.0%; Score 578; DB 11; Length 104;

Best Local Similarity 100.0%; Pred. No. 9, 8e-59; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLTNRDVDCNIMSTNLFHCKDKNTFYSPBPVKAICKGLIISKVLT 60  
DB 1 QDWLTFQKXHLTNRDVDCNIMSTNLFHCKDKNTFYSPBPVKAICKGLIISKVLT 60  
QY 61 SEFYLSDCNVTSPRCYKYLKKSSTNFTCVTCENQAPVHFGVGHG 104  
DB 61 SEFYLSDCNVTSPRCYKYLKKSSTNFTCVTCENQAPVHFGVGHG 104

## RESULT 2

US-09-948-391A-6  
; Sequence 6, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens  
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant)  
; OTHER INFORMATION: Met(-1) RapIR1)  
US-09-948-391A-6

Query Match 100.0%; Score 578; DB 11; Length 105;  
Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODMLTFOKGLTNTDVCNNIMSTNLFPHCKDKNTFTYSRPEPVKAIKGIISKVLT 60  
DB 2 ODMLTFOKGLTNTDVCNNIMSTNLFPHCKDKNTFTYSRPEPVKAIKGIISKVLT 61  
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

## RESULT 3

US-09-961-400-6  
; Sequence 6, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Rana pipiens  
US-09-961-400-6

Query Match 100.0%; Score 578; DB 11; Length 105;  
Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODMLTFOKGLTNTDVCNNIMSTNLFPHCKDKNTFTYSRPEPVKAIKGIISKVLT 60  
DB 2 ODMLTFOKGLTNTDVCNNIMSTNLFPHCKDKNTFTYSRPEPVKAIKGIISKVLT 61  
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

## RESULT 4

US-09-948-391A-28  
; Sequence 28, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Rana pipiens  
; FEATURE:  
; OTHER INFORMATION: Rana pipiens ribonuclease (RapIR1) Clone 5a1b cDNA  
; OTHER INFORMATION: insert  
US-09-948-391A-28

Query Match 100.0%; Score 578; DB 11; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1.2e-58;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODMLTFOKGLTNTDVCNNIMSTNLFPHCKDKNTFTYSRPEPVKAIKGIISKVLT 60  
DB 24 ODMLTFOKGLTNTDVCNNIMSTNLFPHCKDKNTFTYSRPEPVKAIKGIISKVLT 83  
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

## RESULT 5

US-09-961-400-28  
; Sequence 28, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17

;; PRIOR APPLICATION NUMBER: PCT/US99/06641  
;; PRIOR FILING DATE: 1999-03-26  
;; PRIOR APPLICATION NUMBER: 60/079,751  
;; PRIOR FILING DATE: 1998-03-26  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 28  
;; LENGTH: 127  
;; TYPE: PRT  
;; ORGANISM: Rana pipiens  
US-09-961-400-28

Query Match 100.0%; Score 578; DB 11; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1,2e-58;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
Db 24 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 83  
Qy 61 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 104  
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 127

RESULT 6  
US-09-961-400-9  
;; Sequence 9, Application US/09961400  
;; Publication No. US20030124131A1  
;; GENERAL INFORMATION:  
;; APPLICANT: RYBAK, SUSANNA M.  
;; APPLICANT: GOLDBERG, DAVID M.  
;; APPLICANT: NEWTON, DIANNE L.  
;; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
;; FILE REFERENCE: 018733/1059  
;; CURRENT APPLICATION NUMBER: US/09/961,400  
;; CURRENT FILING DATE: 2001-09-25  
;; PRIOR APPLICATION NUMBER: 09/622,613  
;; PRIOR FILING DATE: 2000-08-17  
;; PRIOR APPLICATION NUMBER: PCT/US99/06641  
;; PRIOR FILING DATE: 1999-03-26  
;; PRIOR APPLICATION NUMBER: 60/079,751  
;; PRIOR FILING DATE: 1998-03-26  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 9  
;; LENGTH: 111  
;; TYPE: PRT  
;; ORGANISM: Rana pipiens  
US-09-961-400-9

Query Match 99.5%; Score 575; DB 11; Length 111;  
Best Local Similarity 99.0%; Pred. No. 2,3e-58;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
Db 8 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 67  
Qy 61 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 104  
Db 68 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 111

RESULT 7  
US-09-948-391A-11  
;; Sequence 11, Application US/09948391A  
;; Publication No. US20030027311A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rybak, Susanna M.  
;; APPLICANT: Newton, Dianne L.  
;; APPLICANT: The United States of America

;; APPLICANT: as represented by The Secretary of the  
;; APPLICANT: Department of Health and Human Services  
;; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
;; FILE REFERENCE: 015280-343110US  
;; CURRENT APPLICATION NUMBER: US/09/948,391A  
;; CURRENT FILING DATE: 2002-05-10  
;; PRIOR APPLICATION NUMBER: US 60/079,751  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
;; PRIOR FILING DATE: 1999-03-26  
;; PRIOR APPLICATION NUMBER: US 09/622,613  
;; PRIOR FILING DATE: 2000-08-17  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 11  
;; LENGTH: 104  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens  
;; OTHER INFORMATION: ribonuclease with Q18Ser substitution  
;; OTHER INFORMATION: (recombinant RnA1 Q18)  
US-09-948-391A-11

Query Match 99.1%; Score 573; DB 11; Length 104;  
Best Local Similarity 100.0%; Pred. No. 3,7e-58;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 61  
Db 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 61  
Qy 62 EFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 104  
Db 62 EFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 104

RESULT 8  
US-09-961-400-11  
;; Sequence 11, Application US/09961400  
;; Publication No. US20030124131A1  
;; GENERAL INFORMATION:  
;; APPLICANT: RYBAK, SUSANNA M.  
;; APPLICANT: GOLDBERG, DAVID M.  
;; APPLICANT: NEWTON, DIANNE L.  
;; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
;; FILE REFERENCE: 018733/1059  
;; CURRENT APPLICATION NUMBER: US/09/961,400  
;; CURRENT FILING DATE: 2001-09-25  
;; PRIOR APPLICATION NUMBER: 09/622,613  
;; PRIOR FILING DATE: 2000-08-17  
;; PRIOR APPLICATION NUMBER: PCT/US99/06641  
;; PRIOR FILING DATE: 1999-03-26  
;; PRIOR APPLICATION NUMBER: 60/079,751  
;; PRIOR FILING DATE: 1998-03-26  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 104  
;; TYPE: PRT  
;; ORGANISM: Rana pipiens  
US-09-961-400-11

Query Match 99.1%; Score 573; DB 11; Length 104;  
Best Local Similarity 100.0%; Pred. No. 3,7e-58;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 61  
Db 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 61  
Qy 62 EFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGHC 104

Db 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104

RESULT 9  
US-09-948-391A-13

Sequence 13, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens  
OTHER INFORMATION: ribonuclease with Met at position 1 and Glu2Ser  
OTHER INFORMATION: substitution (recombinant Met(-1) RapiR1 Q1S)  
US-09-948-391A-13

Query Match 99.1%; Score 573; DB 11; Length 105;  
Best Local Similarity 100.0%; Pred. No. 3.7e-58;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLTTS 61  
DB 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLTTS 62  
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104  
DB 63 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 105

RESULT 10  
US-09-961-400-13

Sequence 13, Application US/09961400  
Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/079,751  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 105  
TYPE: PRT

ORGANISM: Rana pipiens  
US-09-961-400-13

Query Match 99.1%; Score 573; DB 11; Length 105;  
Best Local Similarity 100.0%; Pred. No. 3.7e-58;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLTTS 61  
DB 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLTTS 62  
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104  
DB 63 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 105

RESULT 11  
US-09-948-391A-2

Sequence 2, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
FEATURE:  
OTHER INFORMATION: ribonuclease (RapiR1)  
US-09-948-391A-2

Query Match 98.4%; Score 569; DB 11; Length 104;  
Best Local Similarity 99.0%; Pred. No. 1.1e-57;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLTTS 60  
DB 1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLTTS 60  
QY 61 SEFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104  
DB 61 SEFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104

RESULT 12  
US-09-948-391A-4

Sequence 4, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10



```
;; PRIOR APPLICATION NUMBER: US 60/079,751
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: US 09/622,613
;; PRIOR FILING DATE: 2000-08-17
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
;; OTHER INFORMATION: ribonuclease with Met231eu substitution
;; OTHER INFORMATION: (recombinant RapLRI Met231eu)
US-09-948-391A-4
```

```
Query Match      98.4%; Score 569; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 1.1e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
Db 61 FEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
```

## RESULT 13

```
US-09-961-400-4
;; Sequence 4, Application US/09961400
;; Publication No. US20030124131A1
;; GENERAL INFORMATION:
;; APPLICANT: RYBAK, SUSANNA M.
;; APPLICANT: GOLDBERG, DAVID M.
;; APPLICANT: NEWTON, DIANNE L.
;; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;; TITLE OF INVENTION: CELLS
;; FILE REFERENCE: 018733/1059
;; CURRENT APPLICATION NUMBER: US/09/961,400
;; CURRENT FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: 09/622,613
;; PRIOR FILING DATE: 2000-08-17
;; PRIOR APPLICATION NUMBER: PCT/US99/06641
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: 60/079,751
;; PRIOR FILING DATE: 1998-03-26
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Rana pipiens
US-09-961-400-4
```

```
Query Match      98.4%; Score 569; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 1.1e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
Db 61 FEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
```

```
RESULT 14
US-09-961-400-8
```

```
;; Sequence 8, Application US/09961400
;; Publication No. US20030124131A1
;; GENERAL INFORMATION:
;; APPLICANT: RYBAK, SUSANNA M.
;; APPLICANT: GOLDBERG, DAVID M.
;; APPLICANT: NEWTON, DIANNE L.
;; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;; TITLE OF INVENTION: CELLS
;; FILE REFERENCE: 018733/1059
;; CURRENT APPLICATION NUMBER: US/09/961,400
;; CURRENT FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: 09/622,613
;; PRIOR FILING DATE: 2000-08-17
;; PRIOR APPLICATION NUMBER: PCT/US99/06641
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: 60/079,751
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Rana pipiens
US-09-961-400-8
```

```
Query Match      97.8%; Score 565; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.1e-57;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 2 QDWLTFQKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 61
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
Db 62 FEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 105
```

## RESULT 15

```
US-09-948-391A-8
;; Sequence 8, Application US/09948391A
;; Publication No. US20030027311A1
;; GENERAL INFORMATION:
;; APPLICANT: Rybak, Susanna M.
;; APPLICANT: Newton, Dianne L.
;; APPLICANT: as represented by The Secretary of the
;; APPLICANT: Department of Health and Human Services
;; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;; FILE REFERENCE: 015280-134110US
;; CURRENT APPLICATION NUMBER: US/09/948,391A
;; CURRENT FILING DATE: 2002-05-10
;; PRIOR APPLICATION NUMBER: US 60/079,751
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: US 09/622,613
;; PRIOR FILING DATE: 2000-08-17
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 8
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
;; OTHER INFORMATION: ribonuclease with Met at position 1 and Met231eu
;; OTHER INFORMATION: substitution (recombinant Met(-1) RapLRI Met231eu)
US-09-948-391A-8
```

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Query Match      96.9%; Score 560; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.2e-56;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

OY 1 ODMLTFOKHLINTRPVDCNNIMSTNLFHCKDKNTEIYSRPEPVKAICKGIASKVLT 60  
Db 2 ODMLTFOKHLINTRPVDCNNILSTNLFHCKDKNTEIYSRPEPVKAICKGIASKVLT 61  
OY 61 SEFYLSDCNVTSRPCKYKXKSKSTNTFCVTCENOAPVHFVGVGHC 104  
Db 62 FEFYLSDCNVTSRPCKYKXKSKSTNTFCVTCENOAPVHFVGVGHC 105

Search completed: January 22, 2004, 12:12:25  
Job time : 25.7341 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 25.7079 Seconds  
(without alignments)  
1043.940 Million cell updates/sec

Title: US-09-622-613C-2  
Perfect score: 578  
Sequence: 1 QDWLTFQKXHLTNRDVCN.....TFCVTCEQNAQHFVGVGHG 104

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPTRMBL\_23:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578	100.0	127	0918V8	0918V8 rana pipien
2	556	96.2	127	08UVX5	08UVX5 rana pipien
3	404.5	70.0	129	09DFY6	09DFY6 rana pipien
4	386	66.8	128	09DFY8	09DFY8 rana pipien
5	311	53.8	128	09DFY7	09DFY7 rana pipien
6	309	53.5	128	09DFY5	09DFY5 rana pipien
7	298	51.6	133	098SM0	098SM0 rana pipien
8	292	50.5	133	098SM1	098SM1 rana pipien
9	286	49.5	133	098SM2	098SM2 rana pipien
10	282	48.8	133	098SM3	098SM3 rana pipien
11	280	48.4	132	098SM4	098SM4 rana pipien
12	275.5	47.7	132	098SM5	098SM5 rana pipien
13	157.5	27.2	129	09W738	09W738 xenopus lae
14	129	22.3	152	09UK15	09UK15 mus saxicol
15	127	22.0	157	09UK19	09UK19 meriones un

17	126.5	21.9	153	11	09UK17	09UK17 mus saxicol
18	126	21.8	157	11	09UK13	09UK13 meriones un
19	125	21.6	157	11	09UK14	09UK14 meriones un
20	123	21.3	154	11	09UK18	09UK18 mus saxicol
21	122	21.1	157	11	09UK01	09UK01 meriones un
22	121	20.9	157	11	09UK02	09UK02 meriones un
23	120.5	20.8	155	11	09UK09	09UK09 mus pahari
24	119.5	20.7	155	11	09UK13	09UK13 mus saxicol
25	116.5	20.2	155	11	09UK16	09UK16 mus saxicol
26	115.5	20.0	132	6	09TV25	09TV25 eulemur ful
27	115.5	20.0	155	11	09UK12	09UK12 mus saxicol
28	115.5	20.0	155	11	09UK14	09UK14 mus saxicol
29	114.5	19.8	170	6	09BE01	09BE01 ceratopithec
30	113.5	19.6	119	6	09TS06	09TS06 ceratopithec
31	113.5	19.6	119	6	09TV32	09TV32 gorilla gor
32	113.5	19.6	132	6	09TV24	09TV24 galago mono
33	113.5	19.6	147	6	08HZ00	08HZ00 pan troglod
34	113.5	19.6	155	11	09UK14	09UK14 ratus norv
35	113	19.6	156	11	09UK06	09UK06 mus caroli
36	113	19.6	156	11	09UK07	09UK07 mus caroli
37	112.5	19.5	119	6	09TV30	09TV30 mus caroli
38	112.5	19.5	155	11	09UK15	09UK15 mus musculu
39	112.5	19.5	155	11	09UK08	09UK08 mus pahari
40	112	19.4	124	6	09TSF2	09TSF2 bos taurus
41	112	19.4	156	11	09UK07	09UK07 mus caroli
42	111.5	19.3	155	11	09UK03	09UK03 mus caroli
43	111	19.2	124	6	09SNR6	09SNR6 bubalus bub
44	111	19.2	156	6	08S004	08S004 lemur catla
45	111	19.2	156	11	09UK04	09UK04 mus caroli

## ALIGNMENTS

RESULT 1  
Q918V8 PRELIMINARY; PRT; 127 AA.

ID Q918V8  
AC Q918V8  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Onconase variant rapLRI precursor.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
3' UTR of unusual length and structure."  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL; AF165133; AAF76935.1; -;  
DR HSSP; P22069; IONC  
DR InterPro; IPR001427; RNAseA.  
DR Pfam; PF00074; RNAseA; 1.  
DR ProDom; PD000535; RNAseA; 1.  
DR SMART; SM00092; RNAse\_PC; 1.  
DR PROSITE; PS00127; RNAse\_PANCREATIC; 1.  
KW SIGNAL.  
FT SIGNAL. 1 23 POTENTIAL.  
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 100.0%; Score 578; DB 13; Length 127;  
Best Local Similarity 100.0%; Pred. No. 4.3e-58;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QDWLTFQKXHLTNRDVCNINIMSTULFCKDKNTPTYSRPEPVKAICKIISKVLT 60  
DB 24 QDWLTFQKXHLTNRDVCNINIMSTULFCKDKNTPTYSRPEPVKAICKIISKVLT 83

QY 61 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 127

RESULT 2

QY 08UVX5 PRELIMINARY; PRT: 127 AA.

AC Q8UVX5; 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Oncocase precursor.  
GN RPR.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liao Y.-D., Wang S.-C.;  
RT "Rana pipiens onconase genomic DNA";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF332139; AAL54383.1; --  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PDD00535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 96.2%; Score 556; DB 13; Length 127;  
Best Local Similarity 96.2%; Pred. No. 1.4e-55;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFOCKHLLTNRDVDCNNIMSTNLFPHCKDKNTFYTSRPPVKAICGIIASKNVLT 60  
DB 24 ODMLTFOCKHLLTNRDVDCNNIMSTNLFPHCKDKNTFYTSRPPVKAICGIIASKNVLT 83

QY 61 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 127

RESULT 3

QY 09DFY6 PRELIMINARY; PRT: 129 AA.

AC Q9DFY6; 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Rana catesbeiana (Bull frog).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
catesbeiana (bullfrog)";  
RL Nucleic Acids Res. 28:4097-4104 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF242555; AAG31441.2; --  
DR HSP; P22069; IONC.  
HSP; P22069; IONC.

DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PDD00535; RNaseA; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
TT CHAIN 24 129 RC-RNASE4\_RIBONUCLEASE.  
SQ SEQUENCE 129 AA; 14724 MW; 826A628B2B10ABDA CRC64;

Query Match 70.0%; Score 404.5; DB 13; Length 129;  
Best Local Similarity 67.6%; Pred. No. 2.5e-38;  
Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 1 ODMLTFOCKHLLTNRDVDCNNIMSTNLFPHCKDKNTFYTSRPPVKAICGIIASKNVLT 60  
DB 24 ODMLTFOCKHLLTNRDVDCNNIMSTNLFPHCKDKNTFYTSRPPVKAICGIIASKNVLT 83

QY 61 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 127

RESULT 4

QY 09DFY8 PRELIMINARY; PRT: 128 AA.

AC Q9DFY8; 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Rana catesbeiana (Bull frog).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
catesbeiana (bullfrog)";  
RL Nucleic Acids Res. 28:4097-4104 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF242553; AAG31439.1; --  
DR HSP; P22069; IONC.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PDD00535; RNaseA; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
TT CHAIN 24 128 RC-RNASE2\_RIBONUCLEASE.  
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52035ECC CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;  
Best Local Similarity 67.3%; Pred. No. 3.1e-36;  
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 ODMLTFOCKHLLTNRDVDCNNIMSTNLFPHCKDKNTFYTSRPPVKAICGIIASKNVLT 60  
DB 24 ODMLTFOCKHLLTNRDVDCNNIMSTNLFPHCKDKNTFYTSRPPVKAICGIIASKNVLT 83

QY 61 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYSDCNVTSRPPCKYKLTSTNFCVTCENQAPVHFVGVGHC 127

RESULT 5

QY 09DFY7

```

ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; Pubmed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2814986082E0587D CRC64;

Query Match 53.8%; Score 311; DB 13; Length 128;
Best Local Similarity 54.8%; Pred. No. 1.1e-27;
Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

OY 1 QDMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTT 60
DB 24 QDMETFOKKHLTDYKVKCDVEMKALFDCKKNTFTFARPPRYOALCKNIKDNNTVLSR 83
OY 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
DB 84 DAVFLPQCKNRKGLPCHYRLDGSNTTICLTCKELPIHFAGVGKC 127

RESULT 6
O9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; Pubmed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2814986082E0587D CRC64;

Query Match 53.8%; Score 311; DB 13; Length 128;
Best Local Similarity 54.8%; Pred. No. 1.1e-27;
Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

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KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE8FD67D266C7C2 CRC64;

Query Match 53.5%; Score 309; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 1.1e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

OY 1 QDMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTT 60
DB 24 QDMETFOKKHLTDYKVKCDVEMKALFDCKKNTFTFARPPRYOALCKNIKDNNTVLSR 83
OY 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
DB 84 DAVFLPQCKNRKGLPCHYRLDGSNTTICLTCKELPIHFAGVGKC 127

RESULT 7
O98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; Pubmed=11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR PROSITE; PS000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.6%; Score 298; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 3.4e-26;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

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OY 1 QDMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTT 60
DB 23 QNMTATFOKKHITNTSSINCVTMDNNIYIYGQCKGNTFTISSATVVKALIGTVI 81
OY 57 VLTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 104
DB 82 VLTSTRFOALNTCTRTSITPRPCPYSSRTENNYICVACENQPVHFGAGIGRC 132

RESULT 8
O9PMR7 PRELIMINARY; PRT; 133 AA.
AC Q9PMR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

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OX NCBI_TaxID=8400;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Liao Y.D., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rc1 gene encoding a cytochrome b-oxidase.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity."
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL; AF039104; AAD10702.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
KM
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 50.5%; Score 292; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 1.6e-25;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 1 QDWLTFOKHLTNRDVDCNNIMSTNLF---HCKDKNTFYSPREPVKALCKGIASKN 56
DB 23 QWMAKFOOKHITNTPISNCNTIMDNIIYVGQCKRVATFIISATVKAICTGVI-MWN 81

OY 57 VLTSEFYLSDC---NNTSRPCYKYLKSTNTFCVTCENQAPVHFGVGHG 104
DB 82 VLSPTFOLDICTRTSITPRCPYSSKRTETNYICVKCENQIPVHPAGIGRC 132

RESULT 9
O98SL9 PRELIMINARY; PRT; 133 AA.
AC O98SL9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull) frog.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OC NCBI_TaxID=8400;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351210; AAK30256.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
KM
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B2654E CRC64;

Query Match 49.5%; Score 286; DB 13; Length 133;
Best Local Similarity 47.7%; Pred. No. 7.9e-25;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

OY 1 QDWLTFOKHLTNRDVDCNNIMSTNLF---HCKDKNTFYSPREPVKALCKGIASKN 56
DB 23 QWMAKFOOKHITNTPISNCNTIMDNIIYVGQCKRVATFIISATVKAICTGVI-MWN 81
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OY 57 VLTSEFYLSDC---VTSRPCYKYLKSTNTFCVTCENQAPVHFGVGHG 104
DB 82 VLSPTFOLDICTRTSITPRCPYSSKRTETNYICVKCENQIPVHPAGIGOC 132

RESULT 10
O98SM2 PRELIMINARY; PRT; 132 AA.
AC O98SM2;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull) frog.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OC NCBI_TaxID=8400;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DE [2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF351207; AAK10253.1; -.
DR EMBL; AF359578; AAL87036.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
KM
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 49.3%; Score 285; DB 13; Length 132;
Best Local Similarity 47.7%; Pred. No. 1e-24;
Matches 53; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

OY 1 QDWLTFOKHLTNRDVDCNNIMSTNLF---HCKDKNTFYSPREPVKALCKGIASKN 56
DB 23 QWMAKFOOKHITNTPISNCNTIMDNIIYVGQCKRVATFIISATVKAICTGVI-MWNSN 81

OY 57 VLTSEFYLSDC---NNTSRPCYKYLKSTNTFCVTCENQAPVHFGVGHG 104
DB 82 VLSPTFOLDICTRTSITPRCPYSSKRTETNYICVKCENQIPVHPAGIGKC 132

RESULT 11
O98SL8 PRELIMINARY; PRT; 133 AA.
AC O98SL8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull) frog.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OC NCBI_TaxID=8400;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DE [2]
RN
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CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RapLr1).  
 CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA  
 CC library. It exhibits differences with Onconase (RTM) at amino acid  
 CC residues 11, 20, 85 and 103. Carboxy terminal end of RapLr1 has a  
 CC covalently bound ligand binding moiety, which can be a L12 antibody  
 CC directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases.

CC Sequence 127 AA;

Query Match 100.0%; Score 578; DB 20; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-62;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60  
 |||||  
 DB 24 QDWLTFQKHLTNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 83  
 |||||  
 OY 61 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 104  
 |||||  
 DB 84 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 127  
 |||||

#### RESULT 4

AA128866  
 ID AAY28866 standard; Protein; 104 AA.

XX AAY28866;

DT 25-JAN-2000 (first entry)

XX Recombinant RapLr1 Met23Leu amino acid sequence.

DE Recombinant Rana pipiens ribonuclease; RapLr1 Met23Leu; covalently bound;  
 KW CD22 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;  
 KM Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KM recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
 KM autoimmune disease.

XX Rana pipiens.  
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 23 /note= "Wild type Met replaced with Leu"

XX MO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;

XX MPI; 1999-610847/52.

XX DR N-PSDB; AA208125.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases -  
 XX Claim 34; Page 56; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLr1)

CC protein with Met23Leu. Carboxy terminal end of recombinant RapLr1 has a  
 CC covalently bound ligand binding moiety, which can be a L12 antibody  
 CC directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases.

CC Sequence 104 AA;

Query Match 99.5%; Score 575; DB 20; Length 104;  
 Best Local Similarity 99.0%; Pred. No. 5.3e-62;  
 Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60  
 |||||  
 DB 1 QDWLTFQKHLTNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60  
 |||||  
 OY 61 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 104  
 |||||  
 DB 61 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 104  
 |||||

#### RESULT 5

AA128869  
 ID AAY28869 standard; Protein; 105 AA.

XX AAY28869;

DT 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RapLr1 Met23Leu-(His)6 protein.

DE Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RapLr1;  
 KW CD22; covalently bound; L12 antibody; ligand binding moiety; RNase;  
 KM cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;  
 KM signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KM cancer; frog; autoimmune disease.

XX Rana pipiens.  
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 1 /note= "Met not found in wild type RapLr1"

FT Misc-difference 24 /note= "Wild type Met replaced with Leu"

XX MO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;

XX MPI; 1999-610847/52.

XX DR N-PSDB; AA208127.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases -  
 XX Claim 4; Page 59; 71pp; English.

CC The present sequence is a recombinant Rana pipiens ribonuclease protein  
CC (RaplR1) with Met at position 1 attached to (His)6 tag and Met24Leu.  
CC Carboxy terminal end of recombinant RapLr1 has a covalently bound ligand  
CC binding moiety, which can be a Ll2 antibody directed against CD22 on  
CC cancerous B cells or human chorionic gonadotrophin (hCG) effective  
CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be  
CC expressed in bacteria without an N-terminal methionine due to the  
CC presence of a signal peptide that is cleaved by bacteria. The soluble  
CC expression of ribonuclease allows the proteins to be fused in-frame with  
CC ligand binding moieties to form cytotoxic fusion proteins. They can be  
CC used for treatment of cancer and autoimmune diseases.

XX Sequence 105 AA;

Query Match 99.5%; Score 575; DB 20; Length 105;  
Best Local Similarity 99.0%; Pred. No. 5,3e-62;

Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 ODMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICGIIASKVLLTT 60  
2 ODMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICGIIASKVLLTT 61

Dy 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
62 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 6

AA28870 ID AAY28870 standard; Protein; 104 AA.

AC AAY28870;

DT 25-JAN-2000 (first entry)

XX Recombinant RapLr1 GlnSer amino acid sequence.

XX Recombinant Rana pipiens ribonuclease: RapLr1 GlnSer; covalently bound;  
KW Ll2 antibody; ligand binding moiety; CD22; cancerous B cell; frog;  
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;  
KW autoimmune disease.

OS Rana pipiens.  
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

PN WO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US06641.

PR 27-MAR-1998; 98US-0079751.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Newton DL, Rybak SM;

XX MPI: 1999-610847/52.

DR N-PSDB; AA208128.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
PT treating cancers, viral infections or autoimmune diseases -

XX Claim 34; Page 60; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)  
CC protein with GlnSer. Carboxy terminal end of recombinant RapLr1 has a  
CC covalently bound ligand binding moiety, which can be a Ll2 antibody

CC directed against CD22 on cancerous B cells or human chorionic  
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
CC ribonucleases can be expressed in bacteria without an N-terminal  
CC methionine due to the presence of a signal peptide that is cleaved by  
CC bacteria. The soluble expression of ribonuclease allows the proteins to  
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
CC proteins. They can be used for treatment of cancer and autoimmune  
CC diseases.

XX Sequence 104 AA;

Query Match 99.1%; Score 573; DB 20; Length 104;  
Best Local Similarity 100.0%; Pred. No. 9,2e-62;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 2 DMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICGIIASKVLLTT 61  
2 DMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICGIIASKVLLTT 61

Dy 62 EPHYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
62 EPHYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 7

AA28871 ID AAY28871 standard; Protein; 105 AA.

AC AAY28871;

DT 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RapLr1 GlnSer amino acid sequence.

XX Recombinant Met(-1) Rana pipiens ribonuclease GlnSer; RapLr1; CD22;  
KW covalently bound; Ll2 antibody; ligand binding moiety; cancerous B cell;  
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
KW autoimmune disease; RNase.

OS Rana pipiens.  
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RapLr1"

FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

PN WO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US06641.

PR 27-MAR-1998; 98US-0079751.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Newton DL, Rybak SM;

XX MPI: 1999-610847/52.

DR N-PSDB; AA208129.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
PT treating cancers, viral infections or autoimmune diseases -

XX Claim 34; Page 61; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)  
CC protein with Met at position 1 and GlnSer. Carboxy terminal end of  
CC recombinant RapLr1 has a covalently bound ligand binding moiety, which  
CC can be a Ll2 antibody directed against CD22 on cancerous B cells or human



XX	Amino acid sequence of a frog ribonuclease protein.
XX	Frog; ribonuclease; rarnpirnase; RNase.
KM	Rana pipiens.
OS	Rana pipiens.
XX	Key
FT	Modified-site Location/Qualifiers 1 /note= "this Gln is autocyclised to pyroglutamic acid"
XX	US6175003-BI.
PN	
PD	16-JAN-2001.
PF	10-SEP-1999; 99US-0394268.
PR	10-SEP-1999; 99US-0394268.
XX	(ALFA-) ALFACELL CORP.
PA	
PI	Saxena SK;
XI	WPI: 2001-167808/17.
DR	
PT	New nucleic acids encoding a ribonuclease (Rnae), useful for the precise targeting of Rnae to a predetermined cell receptor -
PS	Claim 1; Columns 5-6; 7pp; English.
CC	The present sequence represents a frog ribonuclease protein (rarnpirnase) (RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targeting molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of rarnpirnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it might be most effective.
CC	
CC	
SO	Sequence 104 AA;
QY	Query Match 96.2%; Score 556; DB 22; Length 104; Best Local Similarity 96.2%; Fred. No. 1.1e-59; Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
DB	1 QDMTLTPOKHLTNTRDVCNNIMSTNLPHCKDKNTFIYSRPPEVAICGGIIASKNVLT 60 1 QDMTLTFOKHITNTRDVDCDNIMSTNLPHCKADKNFITISREPPVAIAICKGIIASNVLTT 60
QY	61 SEFLSDCNVTSRPKKYKLKKSTNTFCYTGENOAPAHFGVGHC 104      :     :     :     :     :     :    ::  ::  ::  ::  ::  ::  ::   61 SEFLSDCNVTSRPKKYKLKKSTNKFCYTGENOAPHFVGWSC 104
DB	
RESULT 11	
ID	ABG32650 standard; Proteins; 104 AA. ABG32650
XX	ABG32650;
DT	15-NOV-2002 (first entry)
DE	Northern leopard frog rarnpirnase protein.
KM	Northern leopard frog; rarnpirnase; site-directed mutation; ribonuclease.
OS	Rana pipiens.
XX	Rana pipiens.
PN	US6423515-BI.
PD	23-JUL-2002.
XX	

PF	14-OCT-2000; 2000US-0687748.
XX	
PR	10-SEP-1999; 99US-0394268.
XX	
PA	(ALFA-) ALFACE CELL CORP.
XX	
P1	Saxena SK;
XX	
DR	WPI; 2002-664633/71.
PT	
FT	Constructing isolated nucleic acid encoding ribonuclease, by subjecting
PT	desired recombinant plasmid DNA to different site-directed mutations to
PT	produce nucleic acid, using different polymerase chain reaction
PT	protocols -
XX	
PS	Claim 1; Column 5-6; bpp; English.
XX	
CC	The present invention relates to a new method of constructing isolated
CC	nucleic acid encoding ribonuclease protein with N-terminal Met at
CC	position -1 and Glu at position 1, where its Met has been cleaved and
CC	its Glu has been autocyclised. The method of the invention involves
CC	subjecting pET1d-Ronc(Q1,M23L) plasmid DNA to two different
CC	site-directed mutations, each using overlapping PCR protocol. The method
CC	is useful for constructing an isolated nucleic acid encoding the
CC	ribonuclease. The present amino acid sequence represents the northern
CC	leopard frog ranpirinase protein of the invention.
XX	
SQ	Sequence 104 AA;
	Query Match 96.2%; Score 556; DB 23; Length 104;
	Best Local Similarity 96.2%; Pred. No. 1, le-59;
	Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY	1 ODMTTPCKKHLTNTRDVCNNIMSTNLFHCKDKNTFYISRPYPVKAICKGIASKVLLTT 60
DB	1 ODMTTFCKKHITNRDVDCNNIMSTNLFHCKDKNTFYISRPYPVKAICKGIASKVLLTT 60
OY	61 SEFYLSDCNVTSRPCRYKLKKSTNTFCVTCENAPVAFVGSGHC 104
DB	61 SEFYLSDCNVTSRPCRYKLKKSTNTFCVTCENAPVAFVGSGSC 104
	RESULT 12
ID	AAM35126 standard; Protein; 379 AA.
AAW35126	
XX	AAM35126;
AC	
XX	
DT	20-APR-1998 (first entry)
DE	R. pipiens recombinant RNase ronc fusion protein 2.
XX	
KW	RNase A; ribonuclease; cytotoxic; onconase; nonc; immunofusion;
KW	tumour cell growth; frog.
XX	
OS	Rana pipiens.
OS	Synthetic.
PN	WO9731116-A2.
XX	
PD	28-AUG-1997.
XX	
FP	19-FEB-1997; 97WO-US02568.
XX	
PR	21-FEB-1996; 96US-0011800.
XX	
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	
F1	Bogue L, Newton DL, Rybak SM, Wlodawer A;
XX	
WI	WPI; 1997-435168/40.
DR	N-PSDB; AAT94964.
XX	

PT Ribonuclease molecules based on native Oncanase - used for killing  
PT cells, particularly tumour cells  
XX  
XX  
PS Disclosure; Page 68; 90pp; English.  
XX  
CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins  
CC (Rnuc) which are modifications of the Rnase Oncanase (Rnuc) (Rnuc). Such  
CC novel ribonuclease molecules are highly cytotoxic and can be used alone  
CC or to form chemical conjugates or to target recombinant immunofusions.  
CC They are used particularly for decreasing tumour cell growth. They can  
CC also be used for cell separation in vitro by selectively killing unwanted  
CC types of cells, e.g. in bone marrow prior to transplantation into a  
CC patient undergoing marrow ablation by radiation, or for killing leukemia  
CC cells or T-cells that would cause graft versus host disease. The toxins  
CC can also be used to selectively kill unwanted cells in culture. The new  
CC ribonucleases have increased cytotoxic activity compared to ronc and  
CC also lower immunogenicity in humans.  
XX  
SQ Sequence 379 AA;

Query Match 96.2%; Score 556; DB 18; Length 379;  
Best Local Similarity 96.2%; Pred. No. 5.7e-59;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFISRPVPAICGIIASKVLT 60  
DB 26 ODMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFISRPVPAICGIIASKVLT 85  
OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGHC 104  
DB 86 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGSC 129

## RESULT 13

AAR12344

ID AAR12344 standard; protein; 104 AA.

XX AAR12344;

DT 08-AUG-1991 (first entry)

DE Protein with activity against cancer cells.

KW Frog eggs; Tamoxifen; Stelazine; cancer.

OS Rana pipiens.

XX WO9107435-A.

XX 30-MAY-1991.

XX 26-OCT-1990; 90WO-US06185.

XX 18-MAY-1990; 90US-0526314.

XX 13-NOV-1989; 89US-0436141.

XX (ALFA-) ALFACELL CORP.

XX Ardelc WJ, Mikulski SM;

XX WPI; 1991-178059/24.

PT New protein from fertilised eggs of Rana pipiens - active against  
PT cancer cells, esp. in combination with Tamoxifen or Stelazine  
PT (trifluoro-per-azine).

PS Claim 7; Fig 2; 33pp; English.

CC The protein is derived from fertilised frog eggs. It has an iso-  
CC electric point of 9.5 - 10.5, a blocked N-terminal gp. and is free  
CC of carbohydrate. It is active against certain cancer cells. The  
CC combination of the protein and (2-1-p-dimethylaminoethoxyphenyl)-1,  
CC 2-diphenyl-1-butene) citrate salt (tamoxifen) is much more bio-

CC active than the separate entities against human pancreatic ASPC-1  
CC adenocarcinoma, and the combination of protein and (10-[3-(4-methyl  
CC piperazin-1-yl)-propyl]-2-trifluoromethylphenothiazine (Stelazine)  
CC is much more reactive than the separate entities against human sub-  
CC A-549 carcinoma. Activity has also been shown against human adeno-  
CC carcinoma NIH-OVCAR-3 cells, human leukemic HL-60 cells, human  
CC COLO 320 DM cells, human LOX melanoma and human lung squamous car-  
CC cinoma HT-520 cells.  
XX  
SQ Sequence 104 AA;

Query Match 95.7%; Score 553; DB 12; Length 104;  
Best Local Similarity 95.2%; Pred. No. 2.5e-59;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFISRPVPAICGIIASKVLT 60  
DB 1 EDMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFISRPVPAICGIIASKVLT 60  
OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGSC 104

## RESULT 14

AAR47303

ID AAR47303 standard; protein; 104 AA.

XX AAR47303;

DT 25-MAR-2003 (updated)

DT 09-SEP-1994 (first entry)

DE ONCOMASE (pharmaceutical protein).

KW Onconase; pharmaceutical; protein; adenocarcinoma; treatment;  
KW cisplatin; melphalan; adriamycin; ovarian cancer; ovary.

OS Synthetic.

XX WO9403197-A1.

XX 17-FEB-1994.

XX 02-JUL-1993; 93WO-US06357.

XX 30-JUL-1992; 92US-0921180.

XX (ALFA-) ALFACELL CORP.

XX Ardelc WJ, Mikulski SM;

XX WPI; 1994-065396/08.

PT Pharmaceutical comp. Cisplatin, Melphalan or Adriamycin - active  
PT in-vitro against OVCAR-3 human ovarian adenocarcinoma cells

PS Claim 7; Page 13; 18pp; English.

CC This pharmaceutical protein (ONCOMASE) is used in the production of  
CC a bioactive pharmaceutical composition also comprising one of  
CC Cisplatin (cis-diamminedichloroplatinum), Melphalan, (4-(bis-(2-  
CC chloroethyl)amino)-L-phenylamine) or Adriamycin (doxorubicin HCl).  
CC The composition has bioactivity in vitro against OVCAR-3 human  
CC ovarian adenocarcinoma cells.  
CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 104 AA;

Query Match 95.7%; Score 553; DB 15; Length 104;  
Best Local Similarity 95.2%; Pred. No. 2.5e-59;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Search completed: January 22, 2004, 12:06:22  
Job time : 33.7191 secs

QY 1 QDWLTFQKXHLNTRDVCNINIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EDWLTFQKXHLNTRDVCNINIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60  
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 15

AAW00736  
ID AAW00736 standard; protein; 104 AA.

XX AAW00736;

DT 25-MAR-2003 (updated)  
DT 22-MAY-1997 (first entry)

DE Protein derived from frogs eggs.

XX Rana pipiens; ovarian adenocarcinoma NIH-OVCAR03 cell; frog; egg;  
KW submaxillary epidermoid carcinoma A-253 cell; tumour; human;  
KM leukemic HL-60 cell; COLO 320 DM cell; colon adenocarcinoma;  
KM LOX melanoma; lung squamous carcinoma HT-520 cell.

XX Rana pipiens.

XX US5559212-A.

XX 24-SEP-1996.

XX 01-AUG-1994; 94US-0283970.

XX 03-FEB-1992; 92US-0814332.

XX 06-APR-1988; 88US-0178118.

XX 13-NOV-1989; 89US-0436141.

XX 01-AUG-1994; 94US-0283970.

XX (ALFA-) ALFACELL CORP.

XX Ardelc WJ;

XX WPI; 1996-442459/44.

XX New isolated Rana pipiens frog protein - useful for the treatment of  
tumours.

XX Claim 1; Column 8; 7pp; English.

CC This sequence represents a protein which was prepared by homogenisation  
of Rana pipiens frogs eggs. This protein is used for treating tumours  
in humans. Especially this protein was active against human  
submaxillary epidermoid carcinoma A-253 cells, human ovarian  
adenocarcinoma NIH-OVCAR03 cells, human leukemic HL-60 cells, human  
COLO 320 DM cells originally isolated from colon adenocarcinoma, human  
LOX melanoma and human lung squamous carcinoma HT-520 cells.  
(Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 104 AA;

Query Match 95.7%; Score 553; DB 17; Length 104;  
Best local similarity 95.2%; Pred. No. 2.5e-59;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLNTRDVCNINIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EDWLTFQKXHLNTRDVCNINIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60

QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 22, 2004, 12:01:30 ; Search time 12.6644 Seconds  
(without alignments)  
353.031 Million cell updates/sec

Title: US-09-622-613C-2

Perfect score: 578

Sequence: 1 QDWLTFQKHILNTRVDN.....TFCVTENQAPHFVGHC 104

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	96.5	104	1	US-08-467-955-2
2	556	96.2	104	3	US-09-394-268-1
3	556	96.2	104	4	US-09-687-748-1
4	556	96.2	129	3	US-08-875-811-63
5	556	96.2	379	3	US-08-875-811-43
6	553	95.7	104	1	US-08-283-971-1
7	553	95.7	104	1	US-07-921-619-1
8	553	95.7	104	1	US-08-467-955-1
9	553	95.7	104	2	US-08-891-848-13
10	553	95.7	105	3	US-08-875-811-39
11	553	95.7	355	3	US-08-875-811-41
12	553	95.7	358	3	US-08-875-811-51
13	551	95.3	104	3	US-08-875-811-1
14	551	95.3	104	4	US-09-071-672-1
15	551	95.3	106	3	US-08-875-811-28
16	551	95.3	107	3	US-08-875-811-30
17	551	95.3	112	3	US-08-875-811-32
18	551	95.3	251	3	US-08-875-811-59
19	551	95.3	254	3	US-08-875-811-61
20	551	95.3	355	3	US-08-875-811-49
21	551	95.3	355	3	US-08-875-811-57
22	551	95.3	355	3	US-08-875-811-64
23	551	95.3	366	3	US-08-875-811-55
24	548	94.8	104	3	US-09-394-268-2
25	548	94.8	104	4	US-09-687-748-2
26	546	94.5	105	3	US-08-875-811-24
27	546	94.5	105	3	US-08-875-811-26

28	542	93.8	358	3	US-08-875-811-45	Sequence 45, App1
29	542	93.8	365	3	US-08-875-811-53	Sequence 53, App1
30	527	91.2	107	3	US-08-875-811-20	Sequence 20, App1
31	490	84.8	360	3	US-08-875-811-47	Sequence 47, App1
32	483.5	83.7	111	3	US-08-875-811-22	Sequence 22, App1
33	445	77.0	83	3	US-08-875-811-2	Sequence 2, App1
34	445	77.0	83	4	US-09-071-672-3	Sequence 3, App1
35	289	50.0	111	2	US-08-891-848-12	Sequence 12, App1
36	289	50.0	111	3	US-08-875-811-8	Sequence 8, App1
37	217.5	37.6	114	3	US-09-223-118-4	Sequence 4, App1
38	205.5	35.6	114	3	US-09-223-118-2	Sequence 2, App1
39	204.5	35.4	114	3	US-09-223-118-1	Sequence 1, App1
40	202.5	35.0	114	3	US-08-441-629-2	Sequence 3, App1
41	157.5	27.2	169	1	US-08-441-629-2	Sequence 2, App1
42	157.5	27.2	169	3	US-08-776-207-2	Sequence 2, App1
43	157.5	27.2	169	4	US-09-507-773-2	Sequence 2, App1
44	157.5	27.2	169	5	PCT-US95-09172-2	Sequence 2, App1
45	146	25.3	28	3	US-08-875-811-3	Sequence 3, App1

## ALIGNMENTS

RESULT 1  
US-08-467-955-2  
Sequence 2, Application US/08467955  
Patent No. 5728805  
GENERAL INFORMATION:  
APPLICANT: Ardelt Ph.D., Wojciech J.  
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.A.  
STREET: P.O. Box E  
CITY: Short Hills  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07078-0383  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
Application Number: US/08/467,955  
Filing Date: 13-NOV-1989  
CLASSIFICATION: 435  
Prior Application Data:  
Application Number: US 07/178,118  
Filing Date: 06-APR-1988  
Prior Application Data:  
Application Number: US 07/436,141  
Filing Date: 13-NOV-1989  
Prior Application Data:  
Application Number: US 07/814,332  
Filing Date: 03-FEB-1992  
Prior Application Data:  
Application Number: US 08/283,970  
Filing Date: 01-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5007 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-912-9066  
TELEFAX: 201-912-9442  
TELEX: No. 5728805 Applicable  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-2

Query Match 96.5%; Score 558; DB 1; Length 104;  
Best Local Similarity 96.2%; Pred. No. 1.6e-60;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
DB 1 EDMLTFOKKHVTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104

## RESULT 2

US-09-394-268-1  
Sequence 1, Application US/09394268  
Patent No. 6175003  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shaileendra K  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF  
TITLE OF INVENTION: MAKING THEM  
FILE REFERENCE: 5013  
CURRENT APPLICATION NUMBER: US/09/394,268  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-394-268-1

Query Match 96.2%; Score 556; DB 3; Length 104;  
Best Local Similarity 96.2%; Pred. No. 2.9e-60;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
DB 1 ODMLTFOKKHITNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104

## RESULT 3

US-09-687-748-1  
Sequence 1, Application US/09687748  
Patent No. 6423515  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shaileendra K  
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES  
FILE REFERENCE: 5013 US 01  
CURRENT APPLICATION NUMBER: US/09/687,748  
CURRENT FILING DATE: 2000-10-14  
PRIOR APPLICATION NUMBER: 09/394,268  
PRIOR FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-687-748-1

Query Match 96.2%; Score 556; DB 4; Length 104;  
Best Local Similarity 96.2%; Pred. No. 2.9e-60;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
DB 1 ODMLTFOKKHITNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104

## RESULT 4

US-08-875-811-63  
Sequence 63, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-63

Query Match 96.2%; Score 556; DB 3; Length 129;  
Best Local Similarity 96.2%; Pred. No. 3.8e-60;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60  
DB 26 ODMLTFOKKHITNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 85  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 104  
DB 86 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVC 129

RESULT 5  
US-08-875-811-43  
Sequence 43, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 379 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-43

Query Match 96.2%; Score 556; DB 3; Length 379;  
Best Local Similarity 96.2%; Pred. No. 1.6e-59;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLITNRDVCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 60  
DB 26 EDWLTFQKHLITNRDVCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 85

QY 61 SEFYLSDCVNTSRCKYKLLKSTNTFCVTCENAPVHFGVGC 104  
DB 86 SEFYLSDCVNTSRCKYKLLKSTNTFCVTCENAPVHFGVGC 129

RESULT 6  
US-08-283-971-1  
Sequence 1, Application US/08283971  
Patent No. 5529775  
GENERAL INFORMATION:  
APPLICANT: Ardelit Ph.D, Wojciech J.  
APPLICANT: Mikulski, Stanislaw M.  
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark H. Jay, P.C.  
STREET: P.O. Box 020083, General Post Office  
CITY: Brooklyn  
STATE: New York  
COUNTRY: USA  
ZIP: 11202-0002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,971  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/921,180  
FILING DATE: 30-JUL-1992  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5006 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 718-625-0399  
TELEFAX: 718-625-0399  
TELEX: No. 5529775 Applicable  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Embryo  
US-08-283-971-1

Query Match 95.7%; Score 553; DB 1; Length 104;  
Best Local Similarity 95.2%; Pred. No. 6.6e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLITNRDVCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 60  
DB 1 EDWLTFQKHLITNRDVCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 60

QY 61 SEFYLSDCVNTSRCKYKLLKSTNTFCVTCENAPVHFGVGC 104  
DB 61 SEFYLSDCVNTSRCKYKLLKSTNTFCVTCENAPVHFGVGC 104

RESULT 7  
US-07-921-619-1  
Sequence 1, Application US/07921619  
Patent No. 5595734  
GENERAL INFORMATION:  
APPLICANT: Ardelit Ph.D, Wojciech J.  
APPLICANT: Mikulski, Stanislaw M.  
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.C.  
STREET: P.O. Box 020083, General Post Office  
CITY: Brooklyn  
STATE: New York

COUNTRY: USA  
ZIP: 11202-0002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/921,619  
FILING DATE: 19920728  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5005 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 718-625-0399  
TELEFAX: 718-625-0399  
TELEX: No. 5595734 Applicab  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Embryo  
US-07-921-619-1

Query Match 95.7%; Score 553; DB 1; Length 104;  
Best Local Similarity 95.2%; Pred. No. 6,6e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ODMLTFOKKHLLNTDNDVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60  
DB 1 EDMLTFOKKHLLNTDNDVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 8  
US-08-467-955-1  
Sequence 1, Application US/08467955  
Patent No. 5728805  
GENERAL INFORMATION:  
APPLICANT: Ardelet Ph.D. Wojciech J.  
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.A.  
STREET: P.O. Box E  
CITY: Short Hills  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07078-0383  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,955  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/814,332  
FILING DATE: 03-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,970  
FILING DATE: 01-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5007 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-912-9066  
TELEFAX: 201-912-0442  
TELEX: No. 5728805 Applicab  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-1

Query Match 95.7%; Score 553; DB 1; Length 104;  
Best Local Similarity 95.2%; Pred. No. 6,6e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ODMLTFOKKHLLNTDNDVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60  
DB 1 EDMLTFOKKHLLNTDNDVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 9  
US-08-891-848-13  
Sequence 13, Application US/08891848  
Patent No. 5955073  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholas, Peter J.  
TITLE OF INVENTION: Selective Rhase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,848  
FILING DATE: No. 5955073 yet assigned  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,462  
FILING DATE: 22-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,082  
FILING DATE: 04-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,195  
FILING DATE: 22-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/510,696  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-110310US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= Onc  
US-08-891-848-13

Query Match 95.7%; Score 553; DB 2; Length 104;  
Best Local Similarity 95.2%; Pred. No. 6.6e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLLTNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAKCGIIASKNVLT 60  
DB 1 EDWLTFQKHLLTNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAKCGIIASKNVLT 60  
QY 61 SEFYLSDCNVTSRPCKYKXKSTNFTFCVTCENQAPVHFVGVC 104  
DB 61 SEFYLSDCNVTSRPCKYKXKSTNFTFCVTCENQAPVHFVGVC 104

RESULT 10  
US-08-875-811-39  
Sequence 39, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Faris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-39

Query Match 95.7%; Score 553; DB 3; Length 105;  
Best Local Similarity 95.2%; Pred. No. 6.7e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLLTNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAKCGIIASKNVLT 60  
DB 2 EDWLTFQKHLLTNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAKCGIIASKNVLT 61  
QY 61 SEFYLSDCNVTSRPCKYKXKSTNFTFCVTCENQAPVHFVGVC 104  
DB 62 SEFYLSDCNVTSRPCKYKXKSTNFTFCVTCENQAPVHFVGVC 105

RESULT 11  
US-08-875-811-41  
Sequence 41, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Farris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-41

Query Match 95.7%; Score 553; DB 3; Length 355;  
Best Local Similarity 95.2%; Pred. No. 3,3e-59;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTQKXHLNTRVDNINMSTNLFHCKDKNTFYISRPPEVKAICKGIASKVLT 60  
DB 252 EDWLTQKXHLNTRVDNINMSTNLFHCKDKNTFYISRPPEVKAICKGIASKVLT 311  
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 104  
DB 312 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 355

RESULT 12  
US-08-875-811-51  
Sequence 51, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Farris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-875-811-51

Query Match 95.7%; Score 553; DB 3; Length 358;  
Best Local Similarity 95.2%; Pred. No. 3,4e-59;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTQKXHLNTRVDNINMSTNLFHCKDKNTFYISRPPEVKAICKGIASKVLT 60  
DB 2 EDWLTQKXHLNTRVDNINMSTNLFHCKDKNTFYISRPPEVKAICKGIASKVLT 61  
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 104  
DB 62 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 105

RESULT 13  
US-08-875-811-1  
Sequence 1, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Farris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label=nonc  
OTHER INFORMATION: /note="native ONCOMASE (Registered  
OTHER INFORMATION: Trademark) from Rana pipiens"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note="Xaa = pyroglutamic acid"

US-08-875-811-1

Query Match 95.3%; Score 551; DB 3; Length 104;  
Best Local Similarity 96.1%; Pred. No. 1.2e-59;  
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DMLTFQKHILNTRVDNCCNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLTTS 61  
DB 2 DMLTFQKHILNTRVDNCCNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLTTS 61  
QY 62 EFLYSDCNVTSRCPCKYKLLKSKSTNTFCVTCENQAPVHFGVGHG 104  
DB 62 EFLYSDCNVTSRCPCKYKLLKSKSTNTFCVTCENQAPVHFGVGHG 104

## RESULT 14

US-09-071-672-1  
Sequence 1, Application US/09071672  
Patent No. 6393276  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Goldenberg, David M.  
TITLE OF INVENTION: Immunotoxins Directed Against Malignant  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071.672  
FILING DATE: 01-MAY-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/046.895  
FILING DATE: 02-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-32510US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = Glu or pyroglutamic acid"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /note= "RNase A derived from  
OTHER INFORMATION: Rana pipiens, "onc protein"  
US-09-071-672-1

Query Match 95.3%; Score 551; DB 4; Length 104;  
Best Local Similarity 96.1%; Pred. No. 1.2e-59;

Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DMLTFQKHILNTRVDNCCNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLTTS 61  
DB 2 DMLTFQKHILNTRVDNCCNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLTTS 61  
QY 62 EFLYSDCNVTSRCPCKYKLLKSKSTNTFCVTCENQAPVHFGVGHG 104  
DB 62 EFLYSDCNVTSRCPCKYKLLKSKSTNTFCVTCENQAPVHFGVGHG 104

## RESULT 15

US-08-875-811-28  
Sequence 28, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875.811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011.800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-28

Query Match 95.3%; Score 551; DB 3; Length 106;  
Best Local Similarity 96.1%; Pred. No. 1.2e-59;  
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DMLTFQKHILNTRVDNCCNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLTTS 61  
DB 4 DMLTFQKHILNTRVDNCCNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLTTS 63  
QY 62 EFLYSDCNVTSRCPCKYKLLKSKSTNTFCVTCENQAPVHFGVGHG 104  
DB 64 EFLYSDCNVTSRCPCKYKLLKSKSTNTFCVTCENQAPVHFGVGHG 106

Search completed: January 22, 2004, 12:10:05

Job time : 12.4644 secs

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XX PI Newton DL, Rybak SM;
XX DR MPI: 1999-610847/52.
XX DR N-PSDB; AA208125.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PS treating cancers, viral infections or autoimmune diseases -
XX PS Claim 34; Page 56; 71pp; English.
XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RapL1)
XX CC protein with Met23Leu. Carboxy terminal end of recombinant RapL1 has a
XX CC covalently bound ligand binding moiety, which can be a Ll2 antibody
XX CC directed against CD22 on cancerous B cells or human chorionic
XX CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
XX CC ribonucleases can be expressed in bacteria without an N-terminal
XX CC methionine due to the presence of a signal peptide that is cleaved by
XX CC bacteria. The soluble expression of ribonuclease allows the proteins to
XX CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX CC proteins. They can be used for treatment of cancer and autoimmune
XX CC diseases.
XX SQ Sequence 104 AA:
XX
XX Query Match 100.0%; Score 577; DB 20; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 4.5e-62;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QDMLTFQKGLNTNTRDVCNNILSTNLFPCCKDKNTFIYSRPPVKAICKGIASKVLT 60
Db 1 QDMLTFQKGLNTNTRDVCNNILSTNLFPCCKDKNTFIYSRPPVKAICKGIASKVLT 60
OY 61 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 104
Db 61 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 104

RESULT 2
AA28869
ID AAY28869 standard; Protein; 105 AA.
AC AAY28869;
XX
XX DT 25-JAN-2000 (first entry)
XX DE Recombinant Met(-1) RapL1 Met23Leu-(His)6 protein.
XX KW Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RapL1;
XX KW CD22; covalently bound; Ll2 antibody; ligand binding moiety; RNase;
XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
XX KW cancer; frog; autoimmune disease.
XX OS Rana pipiens.
XX OS Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
XX FT Misc-difference 1 /note= "Met not found in wild type RapL1"
XX FT Misc-difference 24 /note= "wild type Met replaced with Leu"
XX FT
XX PN WO950398-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US06641.
XX PR 27-MAR-1998; 98US-0079751.
XX PT

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Newton DL, Rybak SM;
XX DR MPI: 1999-610847/52.
XX DR N-PSDB; AA208127.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PS treating cancers, viral infections or autoimmune diseases -
XX PS Claim 4; Page 59; 71pp; English.
XX CC The present sequence is a recombinant Rana pipiens ribonuclease protein
XX CC (RapL1) with Met at position 1 attached to (His)6 tag and Met24Leu.
XX CC Carboxy terminal end of recombinant RapL1 has a covalently bound ligand
XX CC binding moiety, which can be a Ll2 antibody directed against CD22 on
XX CC cancerous B cells or human chorionic gonadotropin (hCG) effective
XX CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be
XX CC expressed in bacteria without an N-terminal methionine due to the
XX CC presence of a signal peptide that is cleaved by bacteria. The soluble
XX CC expression of ribonuclease allows the proteins to be fused in-frame with
XX CC ligand binding moieties to form cytotoxic fusion proteins. They can be
XX CC used for treatment of cancer and autoimmune diseases.
XX SQ Sequence 105 AA:
XX
XX Query Match 100.0%; Score 577; DB 20; Length 105;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-62;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QDMLTFQKGLNTNTRDVCNNILSTNLFPCCKDKNTFIYSRPPVKAICKGIASKVLT 60
Db 2 QDMLTFQKGLNTNTRDVCNNILSTNLFPCCKDKNTFIYSRPPVKAICKGIASKVLT 61
OY 61 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 104
Db 62 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 105

RESULT 3
AA28865
ID AAY28865 standard; Protein; 104 AA.
AC AAY28865;
XX
XX DT 25-JAN-2000 (first entry)
XX DE Rana pipiens liver ribonuclease (RapL1).
XX KW Rana pipiens liver ribonuclease; RapL1; covalently bound; Ll2 antibody;
XX KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
XX KW human chorionic gonadotropin; hCG; recombinant ribonuclease; RNase;
XX KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX OS Rana pipiens.
XX OS
XX OS
XX PN WO950398-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US06641.
XX PR 27-MAR-1998; 98US-0079751.
XX PT (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Newton DL, Rybak SM;
XX DR MPI: 1999-610847/52.
XX DR N-PSDB; AA208124.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PT treating cancers, viral infections or autoimmune diseases -

```

XX Claim 1; Page 55; 71pp; English.

XX The present sequence is Rana pipiens liver ribonuclease (RapLr1)

CC protein. Carboxy terminal end of RapLr1 has a covalently bound

CC ligand binding moiety, which can be a L12 antibody directed against

CC CD22 on cancerous B cells or human chorionic gonadotropin (hCG)

CC effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can

CC be expressed in bacteria without an N-terminal methionine due to the

CC presence of a signal peptide that is cleaved by bacteria. The soluble

CC expression of ribonuclease allows the proteins to be fused in-frame with

CC ligand binding moieties to form cytotoxic fusion proteins. They can be

CC used for treatment of cancer and autoimmune diseases.

XX

SQ Sequence 104 AA;

Query Match 99.7%; Score 575; DB 20; Length 104;

Best Local Similarity 99.0%; Pred. No. 7,9e-62;

Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLTNRFDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

DB 1 QDWLTFQKXHLTNRFDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

QY 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 104

DB 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 104

RESULT 4

AAZ28867 ID AAZ28867 standard; Protein; 105 AA.

XX AAZ28867;

XX 25-JAN-2000 (first entry)

DE Recombinant Met(-1) RapLr1.

XX Recombinant Met(-1) Rana pipiens ribonuclease; RapLr1; CD22; RNase;

KM covalently bound; L12 antibody; ligand binding moiety; cancerous B cell;

KM Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;

KM recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;

KM autoimmune disease.

XX Rana pipiens.

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RapLr1"

XX

XX W09950398-A2.

XX

XX 07-OCT-1999.

XX

XX 26-MAR-1999; 99WO-US06641.

XX

XX 27-MAR-1998; 98US-0079751.

XX

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Newton DL, Rybak SM;

XX

XX WPI; 1999-610847/52.

XX

XX N-PSDB; AAZ08126.

XX

XX New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -

XX

XX Claim 34; Page 57; 71pp; English.

XX

XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLr1)

CC protein with Met at position 1. Carboxy terminal end of recombinant

CC RapLr1 has a covalently bound ligand binding moiety, which can be a L12

CC antibody directed against CD22 on cancerous B cells or human chorionic

CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases.

XX

SQ Sequence 105 AA;

Query Match 99.7%; Score 575; DB 20; Length 105;

Best Local Similarity 99.0%; Pred. No. 8e-62;

Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLTNRFDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

DB 2 QDWLTFQKXHLTNRFDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 61

QY 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 104

DB 62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 105

RESULT 5

AAZ28879 ID AAZ28879 standard; Protein; 127 AA.

XX AAZ28879;

XX 25-JAN-2000 (first entry)

DE Rana pipiens Clone 5a1b ribonuclease.

XX

XX Rana pipiens ribonuclease Clone 5a1b; RapLr1; covalently bound; RNase;

KM L12 antibody; ligand binding moiety; CD22; cancerous B cell; oncogene;

KM Kaposi's Sarcoma; human chorionic gonadotropin; hCG; cancer;

KM recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

KM autoimmune disease.

XX Rana pipiens.

OS

XX

FT Key Location/Qualifiers

FT Peptide 1..23

FT /label= "Signal peptide"

FT /note= "Putative"

FT Protein 24..127

FT /label= Rana\_pipiens\_Clone\_5a1b\_ribonuclease

XX

XX W09950398-A2.

XX

XX 07-OCT-1999.

XX

XX 26-MAR-1999; 99WO-US06641.

XX

XX 27-MAR-1998; 98US-0079751.

XX

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Newton DL, Rybak SM;

XX

XX WPI; 1999-610847/52.

XX

XX N-PSDB; AAZ08136.

XX

XX New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -

XX

XX Disclosure; Page 69; 71pp; English.

XX

XX The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RapLr1).

CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA

CC library. It exhibits differences with Oncase (RTM) at amino acid  
CC residues 11, 20, 85 and 103. Carboxy terminal end of RapLRI has a  
CC covalently bound ligand binding moiety, which can be a Lf2 antibody  
CC directed against CD22 on cancerous B cells or human chorionic  
CC gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant  
CC ribonucleases can be expressed in bacteria without an N-terminal  
CC methionine due to the presence of a signal peptide that is cleaved by  
CC bacteria. The soluble expression of ribonuclease allows the proteins to  
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
CC proteins. They can be used for treatment of cancer and autoimmune  
CC diseases.

XX SQ Sequence 127 AA;  
XX  
XX Query Match 99.7%; Score 575; DB 20; Length 127;  
XX Best Local Similarity 99.0%; Pred. No. 1e-61;  
XX Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODLTFQKHLLNTDNDVDCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 60  
DB 24 ODLTFQKHLLNTDNDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 83  
OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 6  
AA28870 ID AAY28870 standard; Protein; 104 AA.  
XX AC AAY28870;  
XX DT 25-JAN-2000 (first entry)  
XX DE Recombinant RapLRI GlnSer amino acid sequence.  
XX KW Recombinant Rana pipiens ribonuclease; RapLRI GlnSer; covalently bound;  
XX Lf2 antibody; ligand binding moiety; CD22; cancerous B cell; frog;  
XX Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;  
XX autoimmune disease.  
XX OS Rana pipiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"  
XX FT  
XX FT  
XX PN WO9950398-A2.  
XX PD 07-OCT-1999.  
XX PF 26-MAR-1999; 99WO-US06641.  
XX PR 27-MAR-1998; 98US-0079751.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Newton DL, Rybak SM;  
XX DR MPI: 1999-610847/52.  
XX DR N-PSDB; AA208128.  
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
XX PT treating cancers, viral infections or autoimmune diseases -  
XX PS Claim 34; Page 60; 71pp; English.  
XX  
XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLRI)  
XX protein with GlnSer. Carboxy terminal end of recombinant RapLRI has a  
XX covalently bound ligand binding moiety, which can be a Lf2 antibody

CC directed against CD22 on cancerous B cells or human chorionic  
CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
CC ribonucleases can be expressed in bacteria without an N-terminal  
CC methionine due to the presence of a signal peptide that is cleaved by  
CC bacteria. The soluble expression of ribonuclease allows the proteins to  
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
CC proteins. They can be used for treatment of cancer and autoimmune  
CC diseases.

XX SQ Sequence 104 AA;  
XX  
XX Query Match 98.8%; Score 570; DB 20; Length 104;  
XX Best Local Similarity 99.0%; Pred. No. 3.2e-61;  
XX Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMLTFQKHLLNTDNDVDCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 61  
DB 2 DMLTFQKHLLNTDNDVDCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 61  
OY 62 EFLYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 EFLYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 7  
AA28871 ID AAY28871 standard; Protein; 105 AA.  
XX AC AAY28871;  
XX DT 25-JAN-2000 (first entry)  
XX DE Recombinant Met(-1) RapLRI GlnSer amino acid sequence.  
XX KW Recombinant Met(-1) Rana pipiens ribonuclease GlnSer; RapLRI; CD22;  
XX covalently bound; Lf2 antibody; ligand binding moiety; cancerous B cell;  
XX Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
XX autoimmune disease; RNase.  
XX OS Rana pipiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 1 /note= "Met not found in wild type RapLRI"  
XX FT  
XX FT  
XX FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"  
XX FT  
XX PN WO9950398-A2.  
XX PD 07-OCT-1999.  
XX PF 26-MAR-1999; 99WO-US06641.  
XX PR 27-MAR-1998; 98US-0079751.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Newton DL, Rybak SM;  
XX DR MPI: 1999-610847/52.  
XX DR N-PSDB; AA208129.  
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
XX PT treating cancers, viral infections or autoimmune diseases -  
XX PS Claim 34; Page 61; 71pp; English.  
XX  
XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLRI)  
XX protein with Met at position 1 and GlnSer. Carboxy terminal end of  
XX recombinant RapLRI has a covalently bound ligand binding moiety, which  
XX can be a Lf2 antibody directed against CD22 on cancerous B cells or human



DE Amino acid sequence of a frog ribonuclease protein.  
 XX Frog; ribonuclease; ranpirinase; RNase.  
 XX Rana pipiens.  
 OS  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "this Gln is autocyclised to pyroglutamic acid"  
 FT  
 XX US6175003-B1.  
 PN 16-JAN-2001.  
 PD  
 XX 10-SEP-1999; 99US-0394268.  
 PF  
 XX 10-SEP-1999; 99US-0394268.  
 PR 10-SEP-1999; 99US-0394268.  
 XX  
 XX (ALFA-) ALFACELL CORP.  
 PA  
 XX Saxena SK;  
 PI  
 XX WPI; 2001-167808/17.  
 DR  
 XX  
 XX New nucleic acids encoding a ribonuclease (Rnase), useful for the  
 PT precise targeting of Rnase to a predetermined cell receptor -  
 PT  
 XX Claim 1; Columns 5-6; 7pp; English.  
 PS  
 XX The present sequence represents a frog ribonuclease protein (ranpirinase)  
 CC (Rnase). The specification describes a synthetic ribonuclease protein,  
 CC in which the addition of cysteine in the ribonuclease facilitates the  
 CC chemical linking of a targeting molecule by the single reactive  
 CC sulfhydryl group. The specification also describes a method for the  
 CC production of ranpirinase using DNA technology instead of processing  
 CC biological material. The re-engineering of the protein molecule allows  
 CC easier attachment to a targeting molecule thereby making it possible for  
 CC the ribonuclease to be delivered to a particular cell receptor where it  
 CC might be most effective.  
 CC  
 XX Sequence 104 AA:  
 SQ  
 Query Match 95.8%; Score 553; DB 22; Length 104;  
 Best Local Similarity 95.2%; Pred. No. 3.7e-59;  
 Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIASKNVLT 60  
 DB 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIASKNVLT 60  
 QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGHC 104  
 DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGSC 104  
 RESULT 11  
 ABG32650  
 ID ABG32650 standard; Protein; 104 AA.  
 XX  
 AC ABG32650;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 XX Northern leopard frog ranpirinase protein.  
 DE  
 XX Northern leopard frog ranpirinase protein.  
 XX  
 XX Northern leopard frog; ranpirinase; site-directed mutation; ribonuclease.  
 XX  
 OS Rana pipiens.  
 XX  
 XX US6423515-B1.  
 PN  
 XX 23-JUL-2002.  
 PD  
 XX

PF 14-OCT-2000; 2000US-0687748.  
 XX  
 XX 10-SEP-1999; 99US-0394268.  
 XX  
 XX (ALFA-) ALFACELL CORP.  
 PA  
 XX Saxena SK;  
 PI  
 XX WPI; 2002-664633/71.  
 DR  
 XX  
 XX Constructing isolated nucleic acid encoding ribonuclease, by subjecting  
 PT desired recombinant plasmid DNA to different site-directed mutations to  
 PT produce nucleic acid, using different polymerase chain reaction  
 PT protocols -  
 PS  
 XX Claim 1; Column 5-6; 8pp; English.  
 PS  
 XX The present invention relates to a new method of constructing isolated  
 CC nucleic acid encoding ribonuclease protein with N-terminal Met at  
 CC position -1 and Glu at position 1, where its Met has been cleaved and  
 CC its Glu has been autocyclised. The method of the invention involves  
 CC subjecting pERR1d-rOnc(Q1,M23L) plasmid DNA to two different  
 CC site-directed mutations, each using overlapping PCR protocol. The method  
 CC is useful for constructing an isolated nucleic acid encoding the  
 CC ribonuclease. The present amino acid sequence represents the northern  
 CC leopard frog ranpirinase protein of the invention.  
 CC  
 XX Sequence 104 AA:  
 SQ  
 Query Match 95.8%; Score 553; DB 23; Length 104;  
 Best Local Similarity 95.2%; Pred. No. 3.7e-59;  
 Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIASKNVLT 60  
 DB 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIASKNVLT 60  
 QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGHC 104  
 DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGSC 104  
 RESULT 12  
 AAW35126  
 ID AAW35126 standard; Protein; 379 AA.  
 XX  
 AC AAW35126;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 XX R. pipiens recombinant Rnase rOnc fusion protein 2.  
 DE  
 XX Rnase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;  
 KW tumour cell growth; frog.  
 XX  
 OS Rana pipiens.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9731116-A2.  
 PN  
 XX 28-AUG-1997.  
 PD  
 XX 19-FEB-1997; 97WO-US02588.  
 PF  
 XX 21-FEB-1996; 96US-0011800.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Boque L, Newton DL, Rybak SM, Wlodawer A;  
 PI  
 XX WPI; 1997-435168/40.  
 DR  
 XX N-PSDB; AAT94964.  
 DR  
 XX

Ribonuclease molecules based on native Onconase - used for killing PT cells, particularly tumour cells

xx  
xx  
ps      Disclosure; Page 68; 90pp; English.

cc      Sequences AAW3125 to AAW35135 represent recombinant fusion proteins  
cc      (ironc) which are modifications of the RNase Onconase (RTM) (ironc). Such  
cc      novel ribonuclease molecules are highly cytotoxic and can be used alone  
cc      or to form chemical conjugates or to target recombinant immunofusions.  
cc      They are used particularly for decreasing tumour cell growth. They can  
cc      also be used for cell separation in vitro by selectively killing unwanted  
cc      types of cells, e.g. in bone marrow prior to transplantation into a  
cc      patient undergoing marrow ablation by radiation, or for killing leukaemia  
cc      cells or T-cells that would cause graft versus host disease. The toxins  
cc      can also be used to selectively kill unwanted cells in culture. The new  
cc      ribonucleases have increased cytotoxic activity compared to nonc and  
cc      also lower immunogenicity in humans.

**SQ Sequence 379 AA;**

Query Match	95.8%	Score 553	DB 18	Length 379
Best Local Similarity	95.2%	Pred. No. 2e-56		
Matches 99	Conservative 3	Mismatches 2	Indels 0	Gaps 0

Qy	1	QDMLTTPGKKHLLTNTNRDWDVDCNNILSTNLFPHCKDKNTFTYSRPEPVKAKICGIIASKNVLT	60
	:	:	:
Db	26	QDMLTTPGKKHLLTNTNRDWDVDCNNIMSTNLFPHCKDKNTFTYSRPEPVKAKICGIIASKNVLT	85
Qy			
Db	61	SEFLSDCNTNTSRPCCKYKLKKSNTTFCVTCENAPVHFGVGHIC	104
	:	:	:
	86	SEFLSDCNTNTSRPCCKYKLKKSNTTFCVTCENAPVHFGVGHIC	129

## RESULT 13

ID AAW30302 standard; protein; 104 AA.

AC AAW30302;

DT 09-JUN-1998 (first entry)

Recombinant onc protein.

KW human immunodeficiency virus type-1; HIV1; replication.

OS *Rana pipiens*.

XX

FT Modified-site

FT	/note=	"pyroglutamic acid; especially
FT		2-pyrrolidone-5-carboxylic acid or
FT		5-oxo-2-pyrrolidinecarboxylic acid"

PN WO9738112-A1.

PD 16-OCT-1997

PF 04-APR-1997; 97WO-US05675.

PR 04-APR-1996; 96US-0626288.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Ardelt W, Boix E, Vasandani VM, Wu YN, Youle RJ;

DR WPI; 1997-512725/47.

PT1 recombinant OHC protein with glutamine residue at position 1 - useful as anticarcinoma and antiviral agent, also as cell culture selection agent

PS Claim 6; Page 28-29; 35pp; English.

CC This sequence represents a recombinant Onc protein comprising a 104 amino  
CC acid sequence having Gln at position 1. Onc, a ribonuclease from Rana  
CC pipiens oocytes, is known as an antitumour agent (e.g. for treating  
CC pancreatic cancer), and inhibitor of human immunodeficiency virus type-1  
CC replication. It can be used therapeutically or as a cell-culture  
CC selection agent, e.g. to identify gene therapy compositions able to  
CC inhibit tumour growth.

**SQ Sequence 104 AA;**

Query Match	95.7%	Score 553	DB 18	Length 104
Best Local Similarity	95.2%	Pred. No. 4.9e-59		
Matches 99	3	Mismatches 2	Indels 0	Gaps 0

```
QY      1 QDWLTQKQKHLTNTRODVDCNNLTSLNLFHCKDKNTFIYSRPEPVAKICKGIIASKVLT 600
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EDMLTQKQKHLTNTRODVDCNNLTSLNLFHCKDKNTFIYSRPEPVAKICKGIIASKVLT 600
```

Dy      61 SEFYLSDCNVTSRPCCKYLKKSNTFTVCENQAPVHFGVGHC 104  
         |||||  
Db      61 SEFYLSDCNVTSRPFCKYLLKKSTNKFCVTCENQAAPHVFVGVSCT 104

## RESULT 14

ID AAR12344 standard; protein; 104 AA.

AC AAR12344 ;

DT 08-AUG-1991 (first entry)

DE Protein with activity against cancer cells.

KW Frog eggs; Tamoxifen; Stelazine; cancer.

OS *Rana pipiens*.

PN W09107435-A.

PD 30-MAY-1991.

PF 26-OCT-1990; 90WO-US06185

PR 18-MAY-1990; 90US-0526314.

XX

XX

XX

XX

PT new protein from fertilised eggs of Rana pipiens - active against cancer cells, esp. in combination with Tamoxifen or Stelazine (trifluoro-per-azine) .

PS Claim 7; Fig 2; 33pp; English.

CC The protein is derived from fertilised frog eggs. It has an iso-  
CC electric point of 9.5 - 10.5, a blocked N-terminal gp. and is free  
CC of carbohydrates. It is active against certain cancer cells. The  
CC combination of the protein and (z-1-2-dimethylaminoethoxyphenyl)-1,  
CC 2-diphenyl-1-butene) citrate salt (Temoxifen) is much more bio-  
CC active than the separate entities against human pancreatic ASpc-1  
CC adenocarcinoma, and the combination of protein and (10-[3-(4-methyl-  
CC piperazin-1-yl)-propyl]-2-trifluoromethylphenylthio)aziridine (Stelazine)  
CC is much more reactive than the separate entities against human lung  
CC A-549 carcinoma. Activity has also been shown against human sub-  
CC maxillary epidermoid carcinoma A-253 cells, human ovarian adeno-  
CC carcinoma NIH-OV-CAR-3 cells, human leukemic HL-60 cells, human  
CC COLO 320 DM cells, human LOX melanoma and human lung squamous car-





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: January 22, 2004, 12:01:30 (Search time 12.4644 Seconds  
(without alignments)  
353.031 Million cell updates/sec

Title: US-09-622-613C-4

Perfect score: 577  
1 QDMLTFQKHLNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	96.2	104	1 US-08-467-955-2	Sequence 2, Appl1
2	553	95.8	104	3 US-09-394-268-1	Sequence 1, Appl1
3	553	95.8	104	4 US-09-687-748-1	Sequence 1, Appl1
4	553	95.8	129	3 US-08-875-811-63	Sequence 63, Appl1
5	553	95.8	379	3 US-08-875-811-43	Sequence 43, Appl1
6	550	95.3	104	1 US-08-283-971-1	Sequence 1, Appl1
7	550	95.3	104	1 US-07-921-619-1	Sequence 1, Appl1
8	550	95.3	104	1 US-08-467-955-1	Sequence 1, Appl1
9	550	95.3	104	2 US-08-891-848-13	Sequence 13, Appl1
10	550	95.3	104	4 US-09-394-268-2	Sequence 2, Appl1
11	550	95.3	104	3 US-09-687-748-2	Sequence 3, Appl1
12	550	95.3	105	3 US-08-875-811-39	Sequence 39, Appl1
13	550	95.3	355	3 US-08-875-811-61	Sequence 61, Appl1
14	550	95.3	358	3 US-08-875-811-51	Sequence 51, Appl1
15	548	95.0	104	3 US-08-875-811-1	Sequence 1, Appl1
16	548	95.0	104	3 US-09-071-672-1	Sequence 1, Appl1
17	548	95.0	106	3 US-08-875-811-28	Sequence 28, Appl1
18	548	95.0	107	3 US-08-875-811-30	Sequence 30, Appl1
19	548	95.0	112	3 US-08-875-811-32	Sequence 32, Appl1
20	548	95.0	251	3 US-08-875-811-59	Sequence 59, Appl1
21	548	95.0	254	3 US-08-875-811-61	Sequence 61, Appl1
22	548	95.0	355	3 US-08-875-811-49	Sequence 49, Appl1
23	548	95.0	355	3 US-08-875-811-57	Sequence 57, Appl1
24	548	95.0	355	3 US-08-875-811-64	Sequence 64, Appl1
25	548	95.0	356	3 US-08-875-811-55	Sequence 55, Appl1
26	543	94.1	105	3 US-08-875-811-24	Sequence 24, Appl1
27	543	94.1	105	3 US-08-875-811-26	Sequence 26, Appl1

28	539	93.4	358	3 US-08-875-811-45	Sequence 45, Appl1
29	539	93.4	365	3 US-08-875-811-53	Sequence 53, Appl1
30	524	90.8	107	3 US-08-875-811-20	Sequence 20, Appl1
31	487	84.4	360	3 US-08-875-811-47	Sequence 47, Appl1
32	480.5	83.3	111	3 US-08-875-811-22	Sequence 22, Appl1
33	442	76.6	83	4 US-08-875-811-2	Sequence 2, Appl1
34	442	76.6	83	4 US-09-071-672-3	Sequence 3, Appl1
35	426	49.6	111	2 US-08-891-848-12	Sequence 12, Appl1
36	286	49.6	111	3 US-08-875-811-8	Sequence 8, Appl1
37	214.5	37.2	114	3 US-09-223-118-4	Sequence 4, Appl1
38	202.5	35.1	114	3 US-09-223-118-2	Sequence 2, Appl1
39	201.5	34.9	114	3 US-09-223-118-1	Sequence 1, Appl1
40	199.5	34.6	114	3 US-09-223-118-3	Sequence 3, Appl1
41	156.5	27.1	169	1 US-08-441-629-2	Sequence 2, Appl1
42	156.5	27.1	169	3 US-08-776-207-2	Sequence 2, Appl1
43	156.5	27.1	169	4 US-09-507-773-2	Sequence 2, Appl1
44	156.5	27.1	169	5 PCT-US95-09172-2	Sequence 2, Appl1
45	143	24.8	28	3 US-08-875-811-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1  
US-08-467-955-2  
Sequence 2, Application US/08467955  
Patent No. 5728605  
GENERAL INFORMATION:  
APPLICANT: Ardelt Ph.D, Wojciech J.  
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.A.  
STREET: P.O. Box E  
CITY: Short Hills  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07078-0283  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,955  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/814,332  
FILING DATE: 03-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,970  
FILING DATE: 01-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5007 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-912-9066  
TELEFAX: 201-912-0442  
TELEX: No. 5728605 Applicable  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-2

Query Match 96.2%; Score 553; DB 1; Length 104;  
Best Local Similarity 95.2%; Pred. No. 2,4e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Db 1 EDMLTFOKKHVTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104  
Db 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104

## RESULT 2

US-09-394-268-1  
Sequence 1, Application US/09394268  
Patent No. 6175003  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shalendra K  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF  
TITLE OF INVENTION: MAKING THEM  
FILE REFERENCE: 5013  
CURRENT APPLICATION NUMBER: US/09/394,268  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-394-268-1

Query Match 95.8%; Score 553; DB 3; Length 104;  
Best Local Similarity 95.2%; Pred. No. 4,1e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Db 1 ODMLTFOKKHVTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104  
Db 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104

## RESULT 3

US-09-687-748-1  
Sequence 1, Application US/09687748  
Patent No. 6423515  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shalendra K  
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES  
FILE REFERENCE: 5013 US 01  
CURRENT APPLICATION NUMBER: US/09/687,748  
CURRENT FILING DATE: 2000-10-14  
PRIOR APPLICATION NUMBER: 09/394,268  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-687-748-1

Query Match 95.8%; Score 553; DB 4; Length 104;  
Best Local Similarity 95.2%; Pred. No. 4,1e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Db 1 ODMLTFOKKHVTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104  
Db 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104

## RESULT 4

US-08-875-811-63  
Sequence 63, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-63

Query Match 95.8%; Score 553; DB 3; Length 129;  
Best Local Similarity 95.2%; Pred. No. 5,5e-60;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60  
Db 26 ODMLTFOKKHVTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 85  
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 104  
Db 86 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGVC 129

RESULT 5  
US-08-875-811-43  
Sequence 43, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 379 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-43

Query Match 95.8%; Score 553; DB 3; Length 379;  
Best Local Similarity 95.2%; Pred. No. 2.3e-59;  
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKNVLT 60  
DB 26 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKNVLT 85  
QY 61 SEFLSDCNVTSRRCCKTKLKSTNTFCVTCENQAPVHFVGHC 104  
DB 86 SEFLSDCNVTSRRCCKTKLKSTNTFCVTCENQAPVHFVGSC 129

RESULT 6  
US-08-283-971-1  
Sequence 1, Application US/08283971  
Patent No. 5529775  
GENERAL INFORMATION:  
APPLICANT: Ardelit Ph.D, Wojciech J.  
APPLICANT: Mikulski, Stanislaw M.  
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark H. Jay, P.C.  
STREET: P.O. Box 020083, General Post Office  
CITY: Brooklyn  
STATE: New York  
COUNTRY: USA  
ZIP: 11202-0002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,971  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/921,180  
FILING DATE: 30-JUL-1992  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5006 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 718-625-0399  
TELEFAX: 718-625-0399  
TEXT: No. 5529775 Applicable  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Embryo  
US-08-283-971-1

Query Match 95.3%; Score 550; DB 1; Length 104;  
Best Local Similarity 94.2%; Pred. No. 9.6e-60;  
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKNVLT 60  
DB 1 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKNVLT 60  
QY 61 SEFLSDCNVTSRRCCKTKLKSTNTFCVTCENQAPVHFVGHC 104  
DB 61 SEFLSDCNVTSRRCCKTKLKSTNTFCVTCENQAPVHFVGSC 104

RESULT 7  
US-07-921-619-1  
Sequence 1, Application US/07921619  
Patent No. 5595734  
GENERAL INFORMATION:  
APPLICANT: Ardelit Ph.D, Wojciech J.  
APPLICANT: Mikulski, Stanislaw M.  
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.C.  
STREET: P.O. Box 020083, General Post Office  
CITY: Brooklyn  
STATE: New York

COUNTRY: USA  
ZIP: 11202-0002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/921,619  
FILING DATE: 19920728  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5005 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 718-625-0399  
TELEFAX: 718-625-0399  
TELEX: No. 5595734 Applicable  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Embryo  
US-07-921-619-1

Query Match 95.3%; Score 550; DB 1; Length 104;  
Best Local Similarity 94.2%; Pred. No. 9,6e-60;  
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ODMLFQKHILTNRDVDCNNILSTNLFPHCKDKNTFTYSRPPVPAICGIIASKNVLT 60  
DB 1 EDMLTFQKHILTNRDVDCNNILSTNLFPHCKDKNTFTYSRPPVPAICGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 8  
US-08-467-955-1  
Sequence 1, Application US/08467955  
Patent No. 5728805  
GENERAL INFORMATION:  
APPLICANT: Atdele P.D. Wojciech J.  
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.A.  
STREET: P.O. Box E  
CITY: Short Hills  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07078-0383  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,955  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/814,332  
FILING DATE: 03-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,970  
FILING DATE: 01-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5007 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-912-9066  
TELEFAX: 201-912-0442  
TELEX: No. 5728805 Applicable  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-1

Query Match 95.3%; Score 550; DB 1; Length 104;  
Best Local Similarity 94.2%; Pred. No. 9,6e-60;  
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ODMLFQKHILTNRDVDCNNILSTNLFPHCKDKNTFTYSRPPVPAICGIIASKNVLT 60  
DB 1 EDMLTFQKHILTNRDVDCNNILSTNLFPHCKDKNTFTYSRPPVPAICGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 9  
US-08-891-848-13  
Sequence 13, Application US/08891848  
Patent No. 5955073  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholls, Peter J.  
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION:
OTHER INFORMATION: /note= "Onconase from Rana pipiens"
US-08-891-848-13

Query Match      95.3%; Score 550; DB 2; Length 104;
Best Local Similarity 94.2%; Pred. No. 9.6e-60;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ODMLTFOKHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIISKVLT 60
Db      1 ODMLTFOKHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIISKVLT 60

Oy      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 10
US-09-394-268-2
Sequence 2, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shaileendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
OTHER INFORMATION: position 72
US-09-394-268-2
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Query Match      95.3%; Score 550; DB 3; Length 104;
Best Local Similarity 95.2%; Pred. No. 9.6e-60;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy      1 ODMLTFOKHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIISKVLT 60
Db      1 ODMLTFOKHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIISKVLT 60

Oy      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 11
US-09-687-748-2
Sequence 2, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shaileendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
OTHER INFORMATION: position 72
US-09-687-748-2

Query Match      95.3%; Score 550; DB 4; Length 104;
Best Local Similarity 95.2%; Pred. No. 9.6e-60;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy      1 ODMLTFOKHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIISKVLT 60
Db      1 ODMLTFOKHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIISKVLT 60

Oy      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 12
US-08-875-811-39
Sequence 39, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875, 811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-39

Query Match 95.3%; Score 550; DB 3; Length 105;  
Best Local Similarity 94.2%; Pred. No. 9,7e-60;  
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 2 EDMLTFQKKHITNTRDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKVLT 61  
Qy 61 SEFYSDCNVTSRPPCKYKLKSKSTNTFCVTCENQAPVHFVGVGHC 104  
Db 62 SEFYSDCNVTSRPPCKYKLKSKSTNTFCVTCENQAPVHFVGVGSC 105

RESULT 13  
US-08-875-811-41  
Sequence 41, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Miodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875, 811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-41

Query Match 95.3%; Score 550; DB 3; Length 355;  
Best Local Similarity 94.2%; Pred. No. 4,8e-59;  
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKVLT 60  
Db 252 EDMLTFQKKHITNTRDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKVLT 311  
Qy 61 SEFYSDCNVTSRPPCKYKLKSKSTNTFCVTCENQAPVHFVGVGHC 104  
Db 312 SEFYSDCNVTSRPPCKYKLKSKSTNTFCVTCENQAPVHFVGVGSC 355

RESULT 14  
US-08-875-811-51  
Sequence 51, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Luis  
APPLICANT: Miodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875, 811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-51

Query Match	95.3%	Score 550	DB 3	Length 358
Best Local Similarity	94.2%	Pred. No. 4.9e-59		
Matches 98	Conservative 4	Mismatches 2	Indels 0	Gaps 0

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Db	2	EDWLTPEKRIITNTRVDVDCNNIMSTYLFHCKDKNTFTYSRPEPVKAIKGIILASKVLTT	61
Qy	61	SEFLTSDCNTSRPCKYKILKKSTNTFCVTCEENAPHPAFVGVGC	104
Db	62	SEFLTSDCNTSRPCKYKILKKSTNTFCVTCEENAPHPAFVGVGC	105

RESULT 15  
US-08-875-811-1

APPLICANT: Rybak, Susana M.  
 APPLICANT: Newton, Dianne L.  
 APPLICANT: Boque, Luis  
 APPLICANT: Wlodawer, Alexander  
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
 NUMBER OF SEQUENCES: 64  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA

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? NAME/KEY: Protein
? LOCATION: 1..104
? OTHER INFORMATION: /label= nOnc
? OTHER INFORMATION: /note= "native ONCONASE (Registered
? OTHER INFORMATION: Trademark) from Rana pipiens"
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 1
? OTHER INFORMATION: /note= "Xaa = pyroglutamic acid"
? OS-08-875-811-1

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Query Match	95.0%;	Score 548;	DB 3;	Length 104;
Best Local Similarity	95.1%;	Pred. No. 1.7e-59;		
Matches 98;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

Search completed: January 22, 2004, 12:10:06  
Job time : 13.4644 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 24.7341 Seconds

(without alignments)  
869.271 Million cell updates/sec

Title: US-09-622-613c-4

Perfect score: 577  
Sequence: 1 QDWLTPQKHLLTNTRDVDCN.....TFCVTCENQAPVHFVGHC 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	100.0	111	11	US-09-961-400-9
2	575	99.7	104	11	US-09-961-400-2
3	575	99.7	105	11	US-09-948-391A-6
4	575	99.7	105	11	US-09-961-400-6
5	575	99.7	127	11	US-09-948-391A-28
6	575	99.7	127	11	US-09-961-400-28
7	571	99.0	104	11	US-09-948-391A-4
8	571	99.0	104	11	US-09-961-400-4
9	570	98.8	104	11	US-09-948-391A-11
10	570	98.8	104	11	US-09-961-400-11
11	570	98.8	105	11	US-09-948-391A-13
12	570	98.8	105	11	US-09-961-400-13
13	567	98.3	105	11	US-09-961-400-8
14	566	98.1	104	11	US-09-948-391A-2
15	562	97.4	105	11	US-09-948-391A-8

16	562	97.4	111	11	US-09-948-391A-9	Sequence 9, Appl1
17	553	95.8	105	15	US-10-153-882-2	Sequence 2, Appl1
18	548	95.0	104	10	US-09-966-119-1	Sequence 1, Appl1
19	548	95.0	104	11	US-09-918-887-1	Sequence 3, Appl1
20	442	76.6	83	10	US-09-986-119-3	Sequence 3, Appl1
21	442	76.6	83	11	US-09-918-887-3	Sequence 3, Appl1
22	279.5	48.4	110	11	US-09-961-400-19	Sequence 19, Appl1
23	279.5	48.4	111	11	US-09-948-391A-21	Sequence 21, Appl1
24	279.5	48.4	111	11	US-09-961-400-21	Sequence 21, Appl1
25	279.5	48.4	117	11	US-09-948-391A-22	Sequence 22, Appl1
26	279.5	48.4	117	11	US-09-961-400-22	Sequence 22, Appl1
27	278.5	48.3	110	11	US-09-948-391A-15	Sequence 15, Appl1
28	278.5	48.3	110	11	US-09-961-400-15	Sequence 15, Appl1
29	278.5	48.3	111	11	US-09-961-400-17	Sequence 17, Appl1
30	273.5	47.4	110	11	US-09-948-391A-19	Sequence 19, Appl1
31	273.5	47.4	110	11	US-09-948-391A-24	Sequence 24, Appl1
32	273.5	47.4	110	11	US-09-961-400-24	Sequence 24, Appl1
33	273.5	47.4	111	11	US-09-948-391A-26	Sequence 26, Appl1
34	273.5	47.4	111	11	US-09-961-400-26	Sequence 26, Appl1
35	272.5	47.2	111	11	US-09-948-391A-17	Sequence 17, Appl1
36	156.5	27.1	169	13	US-10-016-447-2	Sequence 13, Appl1
37	146	25.3	119	12	US-10-074-978A-139	Sequence 13, Appl1
38	125.5	21.8	124	13	US-10-016-447-5	Sequence 5, Appl1
39	112	19.4	147	9	US-09-286-240-6	Sequence 6, Appl1
40	112	19.4	147	9	US-09-863-777-2	Sequence 2, Appl1
41	112	19.4	147	10	US-09-731-872-254	Sequence 254, App
42	112	19.4	147	12	US-09-876-997-254	Sequence 8, Appl1
43	109	18.9	124	10	US-09-981-286A-8	Sequence 141, App
44	103.5	17.9	99	12	US-10-074-978A-141	Sequence 143, App
45	101.5	17.6	89	12	US-10-074-978A-143	

## ALIGNMENTS

RESULT 1	
US-09-961-400-9	
Sequence 9, Application US/09961400	
Publication No. US20030124131A1	
GENERAL INFORMATION:	
APPLICANT: RYBAK, SUSANNA M.	
APPLICANT: GOLDENBERG, DAVID M.	
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT	
FILE REFERENCE: 018733/1059	
CURRENT FILING DATE: 2001-09-25	
PRIOR FILING DATE: 2000-08-17	
PRIOR APPLICATION NUMBER: 09/622,613	
PRIOR FILING DATE: 2000-08-17	
PRIOR APPLICATION NUMBER: PCT/US99/06641	
PRIOR FILING DATE: 1999-03-26	
PRIOR APPLICATION NUMBER: 60/079,751	
PRIOR FILING DATE: 1998-03-26	
NUMBER OF SEQ ID NOS: 43	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 9	
LENGTH: 111	
TYPE: PRT	
ORGANISM: Rana pipiens	
US-09-961-400-9	
Query Match: 100.0%; Score 577; DB 11; Length 111;	
Best Local Similarity 100.0%; Pred. No. 2,4e-58;	
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	8 QDWLTPQKHLLTNTRDVDCNIIISTNLPHCKDKRTFYISREPPKALCKGIASKNVLT 67
QY	61 SEFYLSDCNVTSRPCKYKLLKXSTNTPFCVTCENQAPVHFVGHC 104
DB	68 SEFYLSDCNVTSRPCKYKLLKXSTNTPFCVTCENQAPVHFVGHC 111



RESULT 2  
US-09-961-400-2  
; Sequence 2, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Rana pipiens  
US-09-961-400-2

Query Match 99.7%; Score 575; DB 11; Length 104;  
Best Local Similarity 99.0%; Pred. No. 3,8e-58;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 QDMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLTT 60

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 3  
US-09-948-391A-6  
; Sequence 6, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens  
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant  
; OTHER INFORMATION: Met (-1) RapLr1)  
US-09-948-391A-6

Query Match 99.7%; Score 575; DB 11; Length 105;  
Best Local Similarity 99.0%; Pred. No. 3.9e-58;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLTT 60  
DB 2 QDMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLTT 61

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 4  
US-09-961-400-6  
; Sequence 6, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Rana pipiens  
US-09-961-400-6

Query Match 99.7%; Score 575; DB 11; Length 105;  
Best Local Similarity 99.0%; Pred. No. 3.9e-58;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLTT 60  
DB 2 QDMLTFQKHLNTRDVCNNIMSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLTT 61

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 5  
US-09-948-391A-28  
; Sequence 28, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 127  
TYPE: PRT  
ORGANISM: Rana pipiens  
FEATURE:  
OTHER INFORMATION: Rana pipiens ribonuclease (RaplR1) clone 5a1b cDNA  
US-09-948-391A-28

Query Match 99.7%; Score 575; DB 11; Length 127;  
Best Local Similarity 99.0%; Pred. No. 4.8e-58;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 60  
DB 24 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 83  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 6  
US-09-961-400-28  
Sequence 28, Application US/09961400  
Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCOMUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/079,751  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 127  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-961-400-28

Query Match 99.7%; Score 575; DB 11; Length 127;  
Best Local Similarity 99.0%; Pred. No. 4.8e-58;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 60  
DB 24 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 83  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 84 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 7  
US-09-948-391A-4  
Sequence 4, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America

APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens  
OTHER INFORMATION: ribonuclease with Met23Leu substitution  
OTHER INFORMATION: (recombinant RapLR1 Met23Leu)  
US-09-948-391A-4

Query Match 99.0%; Score 571; DB 11; Length 104;  
Best Local Similarity 99.0%; Pred. No. 1.1e-57;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 60  
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 8  
US-09-961-400-4  
Sequence 4, Application US/09961400  
Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCOMUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/079,751  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-961-400-4

Query Match 99.0%; Score 571; DB 11; Length 104;  
Best Local Similarity 99.0%; Pred. No. 1.1e-57;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 60  
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIIASKNVLT 60  
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

DB 61 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 9  
US-09-948-391A-11

Sequence 11, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens  
OTHER INFORMATION: ribonuclease with Glu1ser substitution  
OTHER INFORMATION: (recombinant RapR1 Q1S)  
US-09-948-391A-11

Query Match 98.8%; Score 570; DB 11; Length 104;  
Best Local Similarity 99.0%; Pred. No. 1.4e-57;  
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTTS 61  
DB 2 DWLTFQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTTS 61

QY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 10  
US-09-961-400-11

Sequence 11, Application US/09961400  
Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
CELLS  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/079,751  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 104  
TYPE: PRT

ORGANISM: Rana pipiens  
US-09-961-400-11

Query Match 98.8%; Score 570; DB 11; Length 104;  
Best Local Similarity 99.0%; Pred. No. 1.4e-57;  
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTTS 61  
DB 2 DWLTFQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTTS 61

QY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 11  
US-09-948-391A-13

Sequence 13, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens  
OTHER INFORMATION: ribonuclease with Met at position 1 and Glu1ser  
OTHER INFORMATION: substitution (recombinant Met(-1) RapR1 Q1S)  
US-09-948-391A-13

Query Match 98.8%; Score 570; DB 11; Length 105;  
Best Local Similarity 99.0%; Pred. No. 1.4e-57;  
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTTS 61  
DB 3 DWLTFQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAIKGIASKNVLTTS 62

QY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104  
DB 63 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 12  
US-09-961-400-13

Sequence 13, Application US/09961400  
Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
CELLS  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/079,751  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-961-400-13

Query Match 98.8%; Score 570; DB 11; Length 105;  
Best Local Similarity 99.0%; Pred. No. 1,4e-57;  
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMLTFQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFTISRPPEVPAKICKGIIASKNVLTTS 61  
DB 3 DMLTFQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFTISRPPEVPAKICKGIIASKNVLTTS 62

OY 62 EFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104  
DB 63 EFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 105

## RESULT 13

US-09-961-400-8  
Sequence 8, Application US/09961400  
Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.  
APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
FILE REFERENCE: 018733/1059  
CURRENT APPLICATION NUMBER: US/09/961,400  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/622,613  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/079,751  
PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-961-400-8

Query Match 98.3%; Score 567; DB 11; Length 105;  
Best Local Similarity 98.1%; Pred. No. 3,2e-57;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QDWLTFQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFTISRPPEVPAKICKGIIASKNVLTTS 60  
DB 2 QDWLTFQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFTISRPPEVPAKICKGIIASKNVLTTS 61

OY 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104  
DB 62 SEFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 105

## RESULT 14

US-09-948-391A-2  
Sequence 2, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Recombinant Anti-Tumor Ribase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
FEATURE:  
OTHER INFORMATION: ribonuclease (RaplR1)  
US-09-948-391A-2

Query Match 98.1%; Score 566; DB 11; Length 104;  
Best Local Similarity 98.1%; Pred. No. 4,1e-57;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QDWLTFQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFTISRPPEVPAKICKGIIASKNVLTTS 60  
DB 1 QDWLTFQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFTISRPPEVPAKICKGIIASKNVLTTS 60

OY 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104  
DB 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104

## RESULT 15

US-09-948-391A-8  
Sequence 8, Application US/09948391A  
Publication No. US20030027311A1  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: The United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Recombinant Anti-Tumor Ribase  
FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: US 60/079,751  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: US 09/622,613  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens  
OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu  
OTHER INFORMATION: substitution (recombinant Met(-1) RapR1 Met23Leu)  
US-09-948-391A-8

Query Match 97.4%; Score 562; DB 11; Length 105;  
Best Local Similarity 98.1%; Pred. No. 1,2e-56;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ODMLTFQKHGLNTRDVCNNILSTNLFHCKDKNTPFYSRPEPVKAICKGIIASKXVLT	60
Db	2	ODMLTFQKHGLNTRDVCNNILSTNLFHCKDKNTPFYSRPEPVKAICKGIIASKXVLT	61
Qy	61	SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	104
Db	62	FEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	105

Search completed: January 22, 2004, 12:12:25  
Job time : 24.7341 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 11.6854 Seconds

(without alignments)  
855.901 Million cell updates/sec

Title: US-09-622-613C-4  
Perfect score: 577  
Sequence: 1 ODWLTFOQKHLLTNTRDVDCN.....TFCVTGQAPVHFVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	550	95.3	104	2 A39035	ribonuclease-relat
2	286	49.6	111	2 A27121	ribonuclease-relat
3	282.5	49.0	111	1 JX0120	ribonuclease-relat
4	266.5	46.2	111	2 UX0085	pancreatic ribonuc
5	146	25.3	119	2 S41111	pancreatic ribonuc
6	128	22.2	124	1 NRUI	pancreatic ribonuc
7	125	21.7	125	1 A32474	angiogenin [valida
8	123	21.3	128	1 NRCU	pancreatic ribonuc
9	122	21.1	124	1 NRWHK	pancreatic ribonuc
10	118.5	20.5	145	1 A35932	angiogenin precurs
11	117	20.3	128	1 NRKS	angiogenin precurs
12	116	20.1	125	1 B43825	angiogenin - rabbi
13	116	20.1	128	1 NRGPB	pancreatic ribonuc
14	114	19.6	124	1 NRCB	pancreatic ribonuc
15	113	19.6	124	1 NRYV	pancreatic ribonuc
16	112	19.4	147	1 NRHUG	angiogenin precurs
17	111	19.2	124	1 NRHP	pancreatic ribonuc
18	109.5	19.0	123	1 A43825	angiogenin - pig
19	109	18.9	124	1 NRBOB	pancreatic ribonuc
20	109	18.9	124	1 NRPG	pancreatic ribonuc
21	109	18.9	150	1 NRBO	pancreatic ribonuc
22	108.5	18.8	147	2 I52489	ribonuclease 4 (EC
23	108	18.7	124	2 S08549	ribonuclease - dom
24	108	18.7	128	1 NRHO	pancreatic ribonuc
25	108	18.7	128	1 NRPO	pancreatic ribonuc
26	108	18.7	167	2 S20066	pancreatic-type ri
27	107.5	18.6	155	2 JC6159	eosinophil-associ
28	106	18.4	124	1 NRSH	pancreatic ribonuc
29	106	18.4	124	1 NRPRH	pancreatic ribonuc

30	106	18.4	124	1 NRGPA	pancreatic ribonuc
31	106	18.4	124	2 S07141	pancreatic ribonuc
32	105	18.2	124	1 NRWB	pancreatic ribonuc
33	105	18.2	124	1 NRGN	pancreatic ribonuc
34	104	18.0	124	1 NRGF	pancreatic ribonuc
35	104	18.0	156	2 JC6160	eosinophil-associ
36	102	17.7	124	1 NRDEO	pancreatic ribonuc
37	102	17.7	124	1 NREKN	pancreatic ribonuc
38	102	17.7	124	1 NRCM	pancreatic ribonuc
39	102	17.7	124	1 NRCM	pancreatic ribonuc
40	102	17.7	124	1 NRCMB	pancreatic ribonuc
41	102	17.7	128	1 NRCW2	pancreatic ribonuc
42	101	17.5	124	1 NRYH	pancreatic ribonuc
43	100	17.3	124	1 NRDER	pancreatic ribonuc
44	100	17.3	124	1 NRDEN	pancreatic ribonuc
45	99	17.2	124	1 NRDEF	pancreatic ribonuc

## ALIGNMENTS

## RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C&gt;Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 30-Jun-1993

C:Accession: A39035

J. Ardeli, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 &lt;ARD&gt;

A:Superfamily: pancreatic ribonuclease

## Query Match

Best Local Similarity 95.3%; Score 550; DB 2; Length 104;  
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ODWLTFOQKHLLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT	60
Db	1	EDWLTFOQKHLLTNTRDVDCNNINSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT	60
Qy	61	SEFYLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	104
Db	61	SEFYLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC	104

## RESULT 2

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C&gt;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993

C:Accession: A27121

R.Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi,

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana) &lt;

A:Reference number: A27121; MUID:67299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 &lt;TTT&gt;

A:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

## Query Match

Best Local Similarity 49.6%; Score 286; DB 2; Length 111;  
Matches 53; Conservative 18; Mismatches 32; Indels 8; Gaps 3;

Qy	1	ODWLTFOQKHLLTNTRDVDCNNILSTNLF---HCKDKNTFIYSRPPVKAICKGIASKNV	56
Db	1	ENWATFOQKHIIINTPIINCNTIMDNNTIYIGVGCCKRVNTFIISATTVKAICTGVI-NMN	59

```
Qy      57 VLTTSFYLSDC--NVTSRPCKYLLKSKSTNFCVTCEADAPVHFVGVGHC 104
      ||::||::||::||::||::||::||::||::||::||::||::||::||
Db      60 VLSTTRFQLNCTRTSITPRPCPYSRTEITNYCVKCENGYPVHFAIGIRG 110
```

### RESULT 3

C:Chondroitinase-related sialic acid-binding lectin - Japanese frog  
 C:Species: Rana japonica (Japanese frog)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JX0120  
 R:Kamitaya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nittha, K.; Kawachi, H.; Takayanagi  
 J.; Biochem. 108, 139-143, 1990  
 A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
 A:Reference number: JX0120; MUID:91035319; PMID:2229005  
 A:Accession: JX0120

A: Molecule type: protein  
A: Residues: 1-111 <KAM>  
A: Experimental source: egg  
C: Superfamily: pancreatic ribonuclease  
C: Keywords: lectin; pyrogutemic acid  
F:1 Modified site: pyrrolidone carboxylic acid (Gln) #stratus experimental  
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

## Query Match

Query Match	49.0%	Score 282.5;	DB 1;	Length 111;
Best Local Similarity	44.1%;	Pred. No. 2.2e-21;		
Matches 49;	Conservative 20;	Mismatches 35;	Indels 7;	Gaps 2

```
QY      1 QDWLTQKQKHLTNTRDVCNNIISTNLF---HCKDKNTFIYSRPEPKAICKGITASKN 566
        |||::||:::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      1 QMAKQEKEHIPTNSINCNITIMDKSIYIVGGCCERNTFIISSATTVTKAICSGASTNRN 600
```

```
QY      57 VLTTFSEFYLDG---NTSPCKKYLKKSTNTEFCVTENQAPVHFVGVC 104
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 VLSTRFQLNTRISATAPRCPYNRSRIETNVICVKCENRLPVHFGAGIGRC 111
```

## RESULT 4

pancreatic ribonuclease (EC 3.1.27.5) - bullfrog  
C.Species: Rana catesbeiana (bullfrog)  
C.Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Aug-1994  
C.Accession: JX0085  
R.Nitita, R., Katayama, N.; Okabe, Y.; Iwana, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg  
J. Biochem. 106, 729-735, 1989  
A.Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.  
A.Reference number: JX0085; MUID:90130374; PMID:2613682

A:Molecule type: protein  
 A:Residues: 1-111 <NIT>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: hydrolase; pyroglutamic acid  
 F11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F110\_35\_104/Active site: His, Lys, His #status predicted  
 F110\_72\_34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match

Query Match	46.2%;	Score 266.5;	DB 2;	Length 11;
Best Local Similarity	42.3%;	Pred. No. 8.8e-20;		
Matches 47;	Conservative 20;	Mismatches 37;	Indels 7;	Gaps 2

[illegible]

## RESULT

RESULT 5  
S41111  
pancreatic ribonuclease - common iguana

C.Species: Iguana iguana (common iguana)  
C.Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Aug-1998  
C.Accession: S4111  
R.Zhao, W. Beintema, J.J. Hofsteenge, J.

A;Reference number: S41111; MUID:94139745; PMID:8307028

A;Molecule type: protein  
A;Residues: 1-119 <ZHA>  
C;Superfamily: pancreatic

Query Match

Query Match	25.3%	Score 146	DB 2	length 119
Best Local Similarity	29.8%	Pred. No. 1.2e-07		
Matches	34	Conservative	44	Indels 16; Gaps 5
			20	Mismatches

```

QY      1  ODWITLTPCKKH-----TNRDVCNNIL-----STNLFHCDDKNTFYSPREPKALC-K 49
Db      1  QDWESFQNKIIDYDTPETSASNPAYCDLMQORRLNPTKCKTRRTFVAHASPSEIQVCGSG 60
QY      50  GIASKRVLTISE-FYISDC-----NITSRCKYKLLKSTNTPCVTCENQAPHF 98
Db      61  GTHYEDNLVDSNESFDLTDCKNKGTAIPSSCKKNGTPGTRIRIRIAENNOQPHF 114

```

## RESULT

pancreatic ribonuclease (EC 3.1.27.5) - *cu1s*  
*N*: Alternate names: RNase 1; RNase A  
*C*: Species: *Galea musteloides* (*cu1s*)  
*C*: Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #ext\_change 04-Oct-1996  
*C*: Accession: A00827  
*R*: Belintema, J.J.; Neuteboom, B.  
*J*: Mol. Evol. 19, 145-152, 1983  
*A*: Title: Origin of the duplicated ribonuclease gene in guinea-pig  
*A*: Reference number: A92957; M0ID:87036770; PMID:6511219

A:Molecule type: protein  
A:Residues: 1-124 <BR>  
A>Note: about one-third of the molecules lacked Ala-1  
C:Comment: The cuts is a rodent belonging to the same subfamily as the guinea pig  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein, hydrolyase, nucleic acid digestion; pancreas  
F:12,41,119/Active site: His\_179, His\_#status predicted  
F:26-84,40-85,-88-110,65-72/Disulfide bonds: #status predicted  
F:94/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match

Query Match	22.2%	Score 128; DB 1;	Length 124;
Best Local Similarity	29.8%	Pred. NO. 0e-06;	
Matches 36; Conservative	19;	Mismatches 34;	Gaps 32;

```

QY      4 LTFKKHL-----TNTEDVDCNNLT---STNLPHCKCKKNTFTYSRPEPVKIKGIIA 53
      5  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      6 MCFQGHMDSDGHPDINTN--YCNEEMVARSMTQGCCKPNTTVHELEAVQAVC-----S 59
      7  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      54 SKNV-----LTTSEFYISDCNVTSRP-----CKYIKAKSKTNTFCVTGCEN--QAPVH 97
      5  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      60 QNIVCEPKNGQTNICYOSHSSMRITTDCKVTSSSKYPNCSYRNTQOKSIIYACCEGTPSVVH 119
      7  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Qy	98	F	98
Db	120	F	120

## RESULT

RESULT 7  
A12474  
angiogenin [validated] - bovine  
N:Alternate names: angiogenesis factor  
N:Contains: ribonuclease (EC 3.1.27.-)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 25-Sep-1989 #sequence\_revision 25-Sep-1989 #text\_change 15-Sep-2000  
C:Accession: A12474; S02001; A30044; S48212

R:Bond, M.D.; Strydom, D.J.  
 Biochemistry 28, 6110-6113, 1989  
 A>Title: Amino acid sequence of bovine angiotensin.  
 A:Reference number: A32474; MUID:89375344; PMID:2757575  
 A:Accession: A32474  
 A:Molecule type: protein  
 A:Residues: 1-125 <BON>  
 A:Experimental source: Plasma  
 R:Maes, P.; Damaré, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tarrar, A.  
 FEBS Lett. 241, 41-45, 1988  
 A>Title: The complete amino acid sequence of bovine milk angiotensin.  
 A:Reference number: S02001; MUID:89065101; PMID:3197838  
 A:Accession: S02001  
 A:Molecule type: protein  
 A:Residues: 1-125 <MA>  
 A:Experimental source: milk  
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
 submitted to the Brookhaven Protein Data Bank, January 1995  
 A:Reference number: A65065; PDB:1AGI  
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms, residues 1-125  
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995  
 A>Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.  
 A:Reference number: A58315; MUID:95224057; PMID:7708754  
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms  
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
 submitted to the Brookhaven Protein Data Bank, April 1996  
 A:Reference number: A65709; PDB:1G10  
 A:Contents: annotation: conformation by (1)H-NMR, residues 1-125  
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
 Biochemistry 35, 8870-8880, 1996  
 A>Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy.  
 A:Reference number: A58821; MUID:96280645; PMID:8688423  
 A:Contents: annotation: conformation by (1)H-NMR  
 R:Reisdorf, C.; Abertel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.  
 Eur. J. Biochem. 224, 811-822, 1994  
 A>Title: Proton resonance assignments and secondary structure of bovine angiotensin.  
 A:Reference number: S48212; MUID:95010071; PMID:7925406  
 A:Contents: annotation: conformation by (1)H-NMR  
 A:Function:  
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation  
 F:60-68/Region: receptor binding #status predicted  
 F:14,41,115/Active site: His, Lys, His #status predicted  
 F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 21.7%; Score 125; DB 1; Length 125;  
 Best Local Similarity 33.0%; Pred. No. 1.6e-05;  
 Matches 32; Conservative 15; Mismatches 32; Indels 18; Gaps 5;

OY 16 DVDGNILSTNLF--HCKDKNFTYRSREPVKAIKGIISKV-----VLITSEFYL 65  
 DB 24 DEYCNMMKMKRLRLPRCKDRTNFHGNKNDIKALCE---DRNGPYRGDLRIKSKSEFOI 79

OY 66 SDC---NVTSR--PCRYKLKSTNFCVTCENQAPVHF 98  
 DB 80 TICGKGGSSRPCKRYGATSDSRVIVGCEGCLPVPHF 116

RESULT 8  
 NRCU  
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Myocastor coypus (nutria, coypu)  
 C>Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
 C:Accession: A00822  
 R:van den Berg, A.; van den Herde-Timmer, L.; Beintema, J.J.  
 Biochim. Biophys. Acta 453, 400-409, 1976  
 A>Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
 A:Reference number: A90612; MUID:77065676; PMID:999896  
 A:Accession: A00822  
 A:Molecule type: protein

A:Residues: 1-128 <VAN>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.3%; Score 123; DB 1; Length 128;  
 Best Local Similarity 29.1%; Pred. No. 2.6e-05;  
 Matches 34; Conservative 19; Mismatches 36; Indels 28; Gaps 7;

OY 6 FOKKIL-----TNTDVDGNIL--STNLF--HCKDKNFTYRSREPVKAIKGIISKV 57  
 DB 8 FERQHMDSRGSPSTPNPCNEMKSRNMTQGRCKKVNFTVHEPLADVQAVC-----FOKIV 63

OY 58 L-----TTSEFYLSDCNVTSRP---CKYKLKSTNFCVTCENQ--APVHF 98  
 DB 64 LCKNGQTCNCGSNMWHITDCRVTSNDPVCNCSYRSTQSEKSIIVACEGNPVVPVHF 120

RESULT 9  
 NRMHK  
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)  
 C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
 C:Accession: A00818  
 R:Emmens, M.; Welling, G.W.; Beintema, J.J.  
 Biochem. J. 157, 317-323, 1976  
 A>Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.  
 A:Reference number: A00818; MUID:76277855; PMID:962870  
 A:Accession: A00818  
 A:Molecule type: protein  
 A:Residues: 1-124 <EM>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
 F:76/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.1%; Score 122; DB 1; Length 124;  
 Best Local Similarity 27.7%; Pred. No. 3.2e-05;  
 Matches 33; Conservative 16; Mismatches 42; Indels 28; Gaps 6;

OY 4 LTFQKHLTNRVD-----CNILSTNLF--HCKDKNFTYRSREPVKAIKGIISKV 55  
 DB 6 MKFORHMDSGNSPNNPNYCNQMMMRKMTQGRCKKPVNTFVHSLFVKAVC---SQK 61

OY 56 NVL-----TTSEFYLSDCNVTSRP---CKYKLKSTNFCVTCENQ--APVHF 98  
 DB 62 NVLCKNGRTNCTYESNSTWHITDCRVTSNDPVCNCSYRSTQSEKSIIVACEGNPVVPVHF 120

RESULT 10  
 A35932  
 angiotensin precursor - mouse  
 N:Alternate names: angiotensin factor  
 N:Contains: ribonuclease (EC 3.1.27.-)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 18-Jun-1999  
 C:Accession: A35932  
 R:Bond, M.D.; Vallee, B.L.  
 Biochem. Biophys. Res. Commun. 171, 988-995, 1990  
 A>Title: Isolation and sequencing of mouse angiotensin DNA.  
 A:Reference number: A35932; MUID:91025023; PMID:2222458  
 A:Accession: A35932  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-145 <BON>  
 A:Cross-references: GB:U022516; NID:g726325; PIDN:AAA91366.1; PID:g726326  
 C:Genetics:  
 A:Introns: #status absent  
 C:Function:



A:Description: hydrolyzes tRNA: induces vascularization of normal and malignant tissues  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid  
F:1-24/Domain: signal sequence #status predicted <Sig>  
F:25-145/Product: angiotensin #status predicted <Mat>  
F:325/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
E:37,64,137/Active site: His, Lys, His #status predicted  
E:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match	20.5%	Score 118.5	DB 1	Length 145
Best Local Similarity	35.5%	Pred No. 8.4e-05		
Matches 27	Conservative 11	Mismatches 31	Indels 7	Gaps 3

30 CKDKTKFIYRPERPVAKIC--KGIISKNV-LTTSELYLSDCVNTS-----RPCKYKLTKKS 82  
 63 CKDQVNTFIHGKNSNIKAICGANGSPRENLKRSKSPFOVTTCHTGGSPRPCCYRASAG 122

QY	83	TNTFCVTCENQAPVHF	98
		:	
Db	123	FRHVVIACENGLPVHF	138

## RESULT 11

pancreatic ribonuclease (BC 3.1.27.5) - castrigua  
C.Species: proechimys guairae (castrigua)  
C.Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 30-Sep-1993  
C.Accession: A00821  
R.Berntema, J.U.; Knoi, G.; Martena, B.  
Biochim. Biophys. Acta 705, 102-110, 1982  
A.Title: The primary structures of pancreatic ribonucleases from African porcupine and e  
A.Reference number: A50644; MUID:83000399; PMID:7115727  
;Accession: A00821

Query Match	20.3%	Score 117;	DB 1;	Length 128;
-------------	-------	------------	-------	-------------

	Matches	34;	Conservative	19;	Mismatches	36;	Indels	28;	Gaps	7
QY	6	FOKKIL-----INTRDVDCNNLT-STNLF--HCKDKNTFYSPREDEVAIKICGIIASKYV	57							
		::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::								
Dd	8	FQRKIDSGSGASTPNPTCNAMMKSRNRITQGECKCPVNTFVHPDLADVQVC---FQKV	63							

```

Qy 58 -----LTTSEFYLSDCVNTR----PCKYKLKSKNTNFCVTCENO-APVHF 98
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 64 PCKNGSNCESTSNMHLTDCRLTSSNSKFPDCLYRTSGEBSILVACEGNPYVPVHF 120

```

RESULT 12

angiogenin - rabbit  
C1Species: *Oryctolagus cuniculus* (domestic rabbit)  
C1Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
R1Accession: S29833; B43825  
R1Bond, M.D.; Strydom, D.J.; Vallee, B.L.  
Biochim. Biophys. Acta 1162, 177-186, 1993  
A1Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discerme  
A1Reference number: S29833; MUID:93192291; PMID:8446182

Query Match Similarity 20.1%; Score 116; DB 1; Length 125;  
Best Local Similarity 31.2%; Pred. No. 0.0013;  
Matches 24; Conservative 13; Mismatches 32; Indels 8; Gaps 3.

Dy 30 CKDKNTFIYSRPEPKAIK---GIASIKV-LTTSEYLSDCNVT-----RPCKYKLKK 81

Db 39 CKDINTFVHGNGKSISKDVCEIDKNGKPYGKINPAISKSFTVTTCKHVGSGSPWPCRYRATS 98

```

QY      82 STNFCVTCENQAPVHF 98
          : ||| |||
Db      99 GSRNIVIACENGLPVHF 115

```

**RESULT 13**

pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)  
N/Alternate names: RNase B  
C/Species: *Cavia porcellus* (guinea pig)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000  
C/Accession: A00826  
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastera, W.; Beintema, J.J.  
E:Biochem. 75, 91-100, 1977  
A>Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure and  
I/Reference number: A91247; PMID:662624; PMID:662624; PMID:7185023; PMID:662624

Query Match	20.1%	Score	116;	DB	1;	Length	128;
Best Local Similarity	27.5%	Pred. No.	0.00013;				
Matches	33;	Conservative	22;	Mismatches	35;	Indels	30;
						Gaps	7

Oy 4 LTPQKHL-----TNTRDVDCNNIL---STNLFHCKDKNTPYSRPEPKAICKGIIAS 54  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 6 MKFQRQHMPDGSPSNSSNY-CNVMIMRRNMTQGRCKRVNTFYHESLADVOAVC----PQ 60

```

Oy 55 KAVL-----TTSEFYLSDCNVTSRP---CKYKLKSTNTFCVTCENQ--APVHF 98
    ||| : ||| ||| : : : ||| |||
Db 61 KAVLCIKNGCOTNCYQSYSRMRITDCRCVTSSSKFPNCSYRMSQAQSKIIVACEGDPYVPVPHF 120

```

## RESULT 14

pancreatic ribonuclease (EC 3.1.27.5) - *Chinchilla brevicaudata* (tentative sequence)  
N:Alternate names: RNase I; RNase A  
C/Species: *Chinchilla brevicaudata*, *Chinchilla lanigera brevicaudata*  
C/Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
C/Accession: A00820  
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
B:Biochim. Biophys. Acta 453, 400-409, 1976  
A:Title: Isolation, properties and primary structure of cypu and chinchilla pancreatic  
A:Reference number: A90612; MUID:77065676; PMID:999896  
A:Accession: A00820

Query Match	19.8%	Score	114	DB	1	Length	124
Best Local Similarity	26.1%	Pred. No.	0.0002				
Matches	31	Conservative	20	Mismatches	40	Indels	28
						Gaps	6



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.23221 Seconds

(without alignments)  
784.758 Million cell updates/sec

Title: US-09-622-613C-4

Perfect score: 577

Sequence: 1 QDWLTFQKHLTNTRDVDCN.....TFCVTCENQAVHFGVGHG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	95.8	104	1	P22069 rana pipien
2	289	50.1	111	1	RNP_O_RANCA
3	282.5	49.0	111	1	P11916 rana catesb
4	266.5	46.2	111	1	P18839 rana japoni
5	146	25.3	119	1	RNPPL_RANCA
6	130.5	22.6	145	1	RNP_IGUIG
7	130.5	22.6	145	1	P80287 iguana igua
8	128	22.2	124	1	ANGI_MOUSE
9	125	21.7	148	1	ANGI_CERAE
10	123	21.3	128	1	RNP_GALMU
11	122	21.1	124	1	RNP_BOVIN
12	121.5	21.1	146	1	ANGI_BOVIN
13	118.5	20.5	145	1	RNP_MYOCO
14	117	20.3	128	1	RNP_BALAC
15	116	20.1	125	1	ANGI_MACMU
16	116	20.1	125	1	ANGI_MOUSE
17	116	20.1	125	1	ANGI_MOUSE
18	114	19.8	124	1	ANGI_MOUSE
19	113	19.6	128	1	ANGI_MOUSE
20	113	19.6	146	1	ANGI_MOUSE
21	113	19.6	146	1	ANGI_MOUSE
22	112	19.4	147	1	ECPI_MOUSE
23	112	19.4	147	1	ANGI_MOUSE
24	111	19.2	124	1	ANGI_MOUSE
25	109.5	19.0	123	1	ANGI_MOUSE
26	109	18.9	124	1	ANGI_MOUSE
27	109	18.9	150	1	RNP_MOUSE
28	109	18.9	150	1	RNP_MOUSE
29	108.5	18.9	156	1	RNP_MOUSE
30	108	18.7	128	1	RNP_MOUSE
31	108	18.7	128	1	RNP_MOUSE
32	108	18.7	128	1	RNP_MOUSE
33	108	18.7	167	1	RNP_MOUSE

## ALIGNMENTS

RESULT 1	ID	QNT0 RANPI	STANDARD	PRT	104 AA
AC	P22069				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OS	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_TaxID=8404;				
RM	[1]				
RP	SEQUENCE.				
RC	TISSUE=Embryo;				
RA	MEDLINE=91093131; PubMed=1985896;				
RA	Ardelt W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens				
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RM	[2]				
RP	3D-STRUCTURE MODELING.				
RC	MEDLINE=9306156; PubMed=1438177;				
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;				
RA	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein:				
RT	a novel antitumor protein of Rana pipiens oocytes and early				
RL	embryos.";				
RL	Proteins 14:392-400(1992).				
RM	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RC	MEDLINE=9416079; PubMed=8120892;				
RA	Mosimann S.C., Ardelt W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an				
RT	amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY				
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR				
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH				
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.				
DR	InterPro: IPR001427; RnaaseA.				
DR	Pfam: PF00074; rnaaseA; 1.				
DR	SMART: SM00092; Rnaase_Pc; 1.				
DR	PROSITE: PS00127; Rnaase_Pc; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure;				
KW	Pyrolydine carboxylic acid.				
FT	MOD_RES	1	1		
FT	ACT_SITE	10	10		
FT	ACT_SITE	31	31		
FT	ACT_SITE	97	97		
FT	DISULFID	19	68		
FT	DISULFID	30	75		

FT DISULFID 48 90  
 FT DISULFID 87 104  
 RT HELIX 3 10  
 FT STRAND 11 12  
 FT HELIX 19 22  
 FT TURN 23 24  
 FT TURN 26 30  
 FT STRAND 33 38  
 FT HELIX 41 45  
 FT HELIX 46 48  
 FT TURN 49 50  
 FT STRAND 55 58  
 FT STRAND 63 70  
 FT TURN 74 75  
 FT STRAND 77 84  
 FT STRAND 86 91  
 FT TURN 92 93  
 FT STRAND 94 101  
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 95.8%; Score 553; DB 1; Length 104;  
 Best Local Similarity 95.2%; Pred. No. 5, 1e-52;  
 Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHILNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIJASKVLT 60  
 DB 1 ODMLTFOKKHILNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIJASKVLT 60  
 OY 61 SEFYLSDCNVTSPCKYKXKSTNFCVTCENQAPVHFGVGHIC 104  
 DB 61 SEFYLSDCNVTSPCKYKXKSTNFCVTCENQAPVHFGVGHIC 104

RESULT 2  
 ID RNPO\_RANCA STANDARD; PRT; 111 AA.  
 AC P11916;

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).  
 DE Rana catesbeiana (Bull. frog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana. OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Egg;  
 RX MEDLINE=8729649; PubMed=3304421;  
 RA Titeani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H., Takeyanagi G., Hakomori S.;  
 RT "Am. no acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";  
 RL Biochemistry 26:2189-2194 (1987).  
 RN [2]  
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.  
 RX MEDLINE=92220613; PubMed=1373237;  
 RA Liao Y.-D.;  
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";  
 RL Nucleic Acids Res. 20:1371-1377 (1992).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC TISSUE=Egg;  
 RX MEDLINE=93192604; PubMed=8448385;  
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H., Takeyanagi Y., Hakomori S., Titeani K.;  
 RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";  
 RL Glycobiology 3:37-45 (1993).  
 RN [4]  
 RP STRUCTURE BY NMR.

RX MEDLINE=96437383; PubMed=9761686;  
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
 RT "The solution structure of a cytoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";  
 RL J. Mol. Biol. 283:231-244 (1998).

CC -1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine residues with a 3' flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin.

CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR: A27121; A27121.

DR PDB: 1BC4; 28-OCT-98.

DR PDB: 1M07; 21-JAN-03.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

KW Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure; PYROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 FT HELIX 3 10  
 FT HELIX 19 23  
 FT TURN 26 27  
 FT STRAND 37 41  
 FT HELIX 45 51  
 FT TURN 52 52  
 FT STRAND 57 62  
 FT STRAND 68 73  
 FT STRAND 83 88  
 FT STRAND 92 97  
 FT TURN 98 99  
 FT STRAND 100 107  
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;

Query Match 50.1%; Score 289; DB 1; Length 111;  
 Best Local Similarity 48.6%; Pred. No. 5, 4e-24;  
 Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

OY 1 ODMLTFOKKHILNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIJASKN 56  
 DB 1 ODMLTFOKKHILNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIJASKN 56  
 OY 57 VLTSEFYLSDC--NVTSPCKYKXKSTNFCVTCENQAPVHFGVGHIC 104  
 DB 60 VLTSEFYLSDC--NVTSPCKYKXKSTNFCVTCENQAPVHFGVGHIC 104

RESULT 3  
 ID LSCS\_RANCA STANDARD; PRT; 111 AA.  
 AC P18839;

DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-).  
 OS Rana japonica (Japanese Reddish frog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana. OX NCBI\_TaxID=8402;  
 RN [1]

RP SEQUENCE, AND DISULFIDE BONDS.  
RC TISSUE=Egg;  
RX MEDLINE=91035319; PubMed=2229005;  
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,  
RT Takayanagi Y., Tltani K.;  
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)  
eggs.";  
RL J. Biochem. 108:139-143(1990).  
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE  
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN  
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT  
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
CC -1- SUBUNIT: Monomer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR HSSP; P11916; 1BC4.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR Prodom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KM Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin;  
KM Pyrolydione carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT ACT\_SITE 10 10 BY SIMILARITY.  
FT ACT\_SITE 35 35 BY SIMILARITY.  
FT ACT\_SITE 104 104 BY SIMILARITY.  
FT DISULFID 19 72 BY SIMILARITY.  
FT DISULFID 34 82  
FT DISULFID 52 97  
FT DISULFID 94 111  
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDP3834ED679 CRC64;  
  
Query Match 49.0%; Score 282.5; DB 1; Length 111;  
Best Local Similarity 44.1%; Pred. No. 2.7e-23;  
Matches 49; Conservative 20; Mismatches 35; Indels 7; Gaps 2;  
  
Qy 1 QDWLTFQKHJLNTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVAKICKGIASKN 56  
Db 1 QWMAFKFKHJLNTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVAKICKGIASKN 60  
1 QWMAFKFKHJLNTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVAKICKGIASKN 60  
57 VLTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTGCENQAPVHFVGVGHC 104  
61 VLTSTRFQNLTCIRDSATAPRCPVNSRTETNIVICVCKENRLEPVHFVGVGHC 111  
  
RESULT 4  
ID RNPL\_RANCA STANDARD; PRT; 111 AA.  
AC P14626;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ribonuclease, liver (EC 3.1.27.5).  
OS Rana catesbeiana (Bull) frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_Taxid=8400;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=90130374; PubMed=2613682;  
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
RT Okazaki T., Ohgi K., Irie M.;  
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)  
liver.";  
RL J. Biochem. 106:729-735(1989).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
CC with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR; JX0085; JX0085.  
DR HSSP; P11916; 1BC4.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR Prodom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KM Hydroxylase; Nuclease; Endonuclease; Pyrolydione carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT ACT\_SITE 10 10 BY SIMILARITY.  
FT ACT\_SITE 35 35 BY SIMILARITY.  
FT ACT\_SITE 104 104 BY SIMILARITY.  
FT DISULFID 19 72 BY SIMILARITY.  
FT DISULFID 34 82 BY SIMILARITY.  
FT DISULFID 52 97 BY SIMILARITY.  
FT DISULFID 94 111 PROBABLE.  
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;  
  
Query Match 46.2%; Score 266.5; DB 1; Length 111;  
Best Local Similarity 42.3%; Pred. No. 1.3e-21;  
Matches 47; Conservative 20; Mismatches 37; Indels 7; Gaps 2;  
  
Qy 1 QDWLTFQKHJLNTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVAKICKGIASKN 56  
Db 1 QWMAFKFKHJLNTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVAKICKGIASKN 60  
1 QWMAFKFKHJLNTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVAKICKGIASKN 60  
57 VLTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTGCENQAPVHFVGVGHC 104  
61 ELSTTSFYLNTCIRDSITPRCPVNSPDNNKICVCKEQQLPVHFVGVGHC 111  
  
RESULT 5  
ID RNPL\_IGUIG STANDARD; PRT; 119 AA.  
AC P80287;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).  
OS Iguana iguana (Common Iguana).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauroidea; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
OX NCBI\_Taxid=8517;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=94139745; PubMed=8307028;  
RA Zhao W., Beintema J.J., Hofsteenge J.;  
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic  
ribonuclease.";  
RL Eur. J. Biochem. 219:641-646(1994).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
CC with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Pancreas.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR HSSP; P00656; 1LSQ.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR Prodom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KM Hydroxylase; Nuclease; Endonuclease; Pyrolydione carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT ACT\_SITE 10 10 BY SIMILARITY.  
FT ACT\_SITE 35 35 BY SIMILARITY.  
FT ACT\_SITE 104 106 BY SIMILARITY.  
FT ACT\_SITE 10 10 BY SIMILARITY.  
FT ACT\_SITE 40 40 BY SIMILARITY.  
FT ACT\_SITE 113 113 BY SIMILARITY.



```

Db      53 TWRRLHLS-----CKDINTFIHGRHRIKACDGENGPYGENLRISK 97
Oy      61 SEFYISDCNVTS-----RCKYKLSKSTNTFCVTGENQAPVH 97
Db      98 SPFOVTCNLGRSGPRPCQYRATGRSRIIVGCEGLFVH 138

RESULT 8
RNP_GALMU
ID      RNP_GALMU      STANDARD;      PRT;      124 AA.
AC      P00680;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN      RNASE1 OR RN51.
OS      Galea musceloides (Cuis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Galea.
OX      NCBI_TaxId=10146;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=87036770; PubMed=6571219;
RA      Beintema J.J., Neuteboom B.;
RT      "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT      of the amino acid sequences with those of two close relatives:
RT      capybara and cuia ribonuclease.";
RL      J. Mol. Evol. 19:145-152(1983).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Pancreas.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR      HSSP; P00656; 1SRN.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaaseA; 1.
DR      PRINTS; PRO0794; RIBONUCLEASE.
DR      PRODOM; PD000535; RNaseA; 1.
DR      SMART; SMO0092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Hydroxylase; Nuclease; Endonuclease.
FT      DISULFID 26
FT      DISULFID 40
FT      DISULFID 58
FT      DISULFID 65
FT      ACT_SITE 12
FT      ACT_SITE 41
FT      ACT_SITE 119
FT      VARIANT 1
SQ      SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.24; Score 128; DB 1; Length 124;
Best Local Similarity 29.81; Pred. No. 7.4e-07;
Matches 36; Conservative 19; Mismatches 34; Indels 32; Gaps 7;

Oy      4 LTFQKGL-----TNRDVCNNIL-----STNLFHCKDKTFTYSPREPKAICKGIIA 53
Db      6 MKPQRQMDSDGHDITN--YCEBEMWRNSMTGRCRCPVTFVHEPLEAVQAVC-----S 59
Oy      54 SKNV-----LTTSEFYISDCNVTSRP-----CKYKLSKSTNTFCVTGEN--QAPVH 97
Db      60 QKQVPCNGQGTNCVQSHSSMRITDCRYTSSSKYPNCGRPMQAQKSIIVACEGTPSPVPH 119
Oy      98 F 98
Db      120 F 120

RESULT 9
ANGI_BOVIN

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ID      ANGI_BOVIN      STANDARD;      PRT;      148 AA.
AC      P10152; O9GKPP9;
DT      01-MAR-1989 (Rel. 10, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Angiogenin-1 precursor (EC 3.1.27.-).
GN      ANGI OR ANG.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxId=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Chang S.-I.;
RT      "Cloning, sequencing, and expression of bovine angiogenin.";
RL      Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN      [2]
RP      SEQUENCE OF 24-148.
RC      TISSUE=Milk;
RX      MEDLINE=89065101; PubMed=3197838;
RA      Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT      "The complete amino acid sequence of bovine milk angiogenin.";
RL      FEBS Lett. 241:41-45(1988).
RN      [3]
RP      SEQUENCE OF 24-148.
RC      TISSUE=Plasma;
RX      MEDLINE=89375344; PubMed=2775757;
RA      Bond M.D., Strydom D.J.;
RT      "Amino acid sequence of bovine angiogenin.";
RL      Biochemistry 28:6110-6113(1989).
RN      [4]
RP      CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC      TISSUE=Plasma;
RX      MEDLINE=89118214; PubMed=3064806;
RA      Bond M.D., Vallee B.L.;
RT      "Isolation of bovine angiogenin using a placental ribonuclease
RT      inhibitor binding assay.";
RL      Biochemistry 27:6282-6287(1988).
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX      MEDLINE=95224057; PubMed=7708754;
RA      Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
RT      "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN      [6]
RP      STRUCTURE BY NMR.
RX      MEDLINE=96280645; PubMed=8688423;
RA      Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT      "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT      resonance spectroscopy.";
RL      Biochemistry 35:8870-8880(1996).
CC      -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC      TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC      ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC      PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD AND
CC      MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC      HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL
CC      RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: SERUM, AND MILK.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).

```





DB 6 MKFORHDSGNSPGNNPNYCNQMMRRKMGRCAPVNTFVHESLEDAVAVC----SQK 61  
 QY 56 NVL-----TSEFLSDCMTNTSR---CKYKLSKSTNTFCYTCENQAPVH 98  
 DB 62 NVLCNGRGTNCYESNSTWHTIDCROTGSSEKYPNCAVKTSSQKSHIIVACEGNPYVPVHF 120

RESULT 12  
 ANGI\_MOUSE STANDARD; PRT; 146 AA.  
 ID ANGI\_MOUSE  
 AC Q8WNG3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNAse 5).  
 GN ANG OR RNASES.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxId=9544;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21918422; PubMed=11919285;  
 RA Zhang J., Rosenberg H.F.;  
 RT "Diverifying selection of the tumor-growth promoter angiogenin in  
 RT primate evolution.";  
 RL Mol. Biol. Evol. 19:438-445(2002).  
 CC - FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS (By similarity).  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - SIMILARITY: Belongs to the pancreatic ribonuclease family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AF441667; AAL61649.1; -  
 CC InterPro; IPR001427; RNaseA.  
 CC Pfam; PF00074; RNaseA; 1.  
 CC Prodom; PD000535; RNaseA; 1.  
 CC SMART; SM00092; RNase\_Pc; 1.  
 CC PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 CC DR Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 CC KW Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.  
 CC FT SIGNAL 1 24  
 CC FT CHAIN 25 146  
 CC FT MOD\_RES 25 25  
 CC FT ACT\_SITE 37 37  
 CC FT ACT\_SITE 64 64  
 CC FT ACT\_SITE 138 138  
 CC FT DISULFID 50 105  
 CC FT DISULFID 63 116  
 CC FT DISULFID 81 131  
 CC SEQUENCE 146 AA; 16301 MW; E39A89215DB2A244 CRC64;

Query Match 21.1%; Score 121.5; DB 1; Length 146;  
 Best Local Similarity 28.7%; Pred. No. 4.3e-06;  
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;  
 OY 5 TFOKKHLNTNTDVCCNLTNTLPHCKDKNTFTYRREPVAIC---KGIASKV-LTT 60  
 DB 53 TMRRLHLSP-----CKDINTFVHGNNRHHTALCGDENGSPYGNLRIST 97

QY 61 SEFLSDCMTNTS---RCKYKLSKSTNTFCYTCENQAPVH 97  
 DB 98 SPFOVTTCKLRGSPRPFCOYRATRGSRNIVVGCENGLPVH 138

RESULT 13  
 ANGI\_MOUSE STANDARD; PRT; 145 AA.  
 ID ANGI\_MOUSE  
 AC P21570;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNAse 5).  
 GN ANG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91025023; PubMed=2222458;  
 RA Bond M.D., Vallee B.L.;  
 RT "Isolation and sequencing of mouse angiogenin DNA.";  
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Serum;  
 RX MEDLINE=8448182;  
 RA Bond M.D., Struydom D.J., Vallee B.L.;  
 RT "Characterization and sequencing of rabbit, pig and mouse  
 RT angiogenins: discernment of functionally important residues and  
 RT regions.";  
 RL Biochim. Biophys. Acta 1162:177-186(1993).

CC - FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; U22516; AAA91366.1; -  
 CC HSR; A35932; A35932.  
 CC HSP; P03950; 1A4Y.  
 CC MGD; MGI:88022; Ang.  
 CC InterPro; IPR001427; RNaseA.  
 CC Pfam; PF00074; RNaseA; 1.  
 CC PRINTS; PR00794; RIBONUCLEASE.  
 CC Prodom; PD000535; RNaseA; 1.  
 CC SMART; SM00092; RNase\_Pc; 1.  
 CC PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 CC KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 CC KW Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.  
 CC FT SIGNAL 1 24  
 CC FT CHAIN 25 145  
 CC FT MOD\_RES 25 25  
 CC FT ACT\_SITE 37 37  
 CC FT ACT\_SITE 64 64  
 CC FT ACT\_SITE 137 137  
 CC FT DISULFID 50 104  
 CC FT DISULFID 63 115

Query Match 21.1%; Score 121.5; DB 1; Length 146;  
 Best Local Similarity 28.7%; Pred. No. 4.3e-06;  
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;  
 OY 5 TFOKKHLNTNTDVCCNLTNTLPHCKDKNTFTYRREPVAIC---KGIASKV-LTT 60  
 DB 53 TMRRLHLSP-----CKDINTFVHGNNRHHTALCGDENGSPYGNLRIST 97

FT	DISULFID	81	130	BY SIMILARITY.
SO	SEQUENCE	145 AA;	16228 MW;	06544260BB764938 CRC64;
	Query Match	20.5%	Score 118.5;	DB 1; Length 145;
	Best Local Similarity	35.5%	Pred. No. 8,9e-06;	
	Matches	27; Conservative	11; Mismatches	31; Indels 7; Gaps 3;
OY		30	CKDKNTFYFSRPEPYKAIC--KGIASKNV-LTTSSEFYLSDCNVTs----	RPCKYKLKKS 82
Db		63	CKDQNTFHHGKNSNKAIICGANGSYRENLRHSKSPFYVTTCKHGTGSGPRPCQYRAASG	122
OY		83	TNTFCVTCEQAPVAHF	98
		:		
Db		123	FRHVVIACENGLPVHF	138

ID	PAPHA	STANDARD:	PRT:	1A6.A.
AC	ANGI_PAPHA_08NMN64;			
DT	28-FEB-2003 (Rel. 41,			
DT	28-FEB-2003 (Rel. 41,	Last sequence update)		
DT	28-FEB-2003 (Rel. 41,	Last annotation update)		
DE	AngioGenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNAse 5).			
GN	ANG OR RNASE5.			
OS	Papilio hamadryas (Hamadryas baboon);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
CC	Cercopithecinae; Papio.			
OK	NCBI_taxid=9357;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21918422; Pubmed=11919285;			
RA	Zhang J., Rosenberg H.F.;			
RT	"Diversifying selection of the tumor-growth promoter angiogenin in primate evolution.";			
RU	Mol. Biol. Evol. 19:438-445(2002).			
CC	- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS. ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (By similarity). - SUBCELLULAR LOCATION: Secreted. - SIMILARITY: Belongs to the pancreatic ribonuclease family.			
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DR	EMBL; AF41666; AAU61648.1; .			
DR	InterPro; IPR001427; RNAseA.			
DR	pfam; PF00074; rnaasea. 1.			
DR	ProDom; PDO000535; RNAseA; 1.			
DR	SMART; SMO0092; RNAse Pc; 1.			
DR	PROSITE; PS00127; RNAse PANCREATIC; 1.			
KM	Hydrolase; Nuclease; Endonuclease; Angiogenesis;			
KM	protein synthesis inhibitor; Signal; Pyrolydone carboxylic acid.			
FT	SIGNAL	1 24		
FT	CHAIN	25 146		
FT	MOD_RES	25 25		
FT	ACT_SITE	37 37		
FT	ACT_SITE	64 64		
FT	ACT_SITE	138 138		
FT	DISTULFID	50 105		
FT	DISTULFID	63 116		
FT	DISTULFID	81 131		

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SQ SEQUENCE 146 AA; 16432 MW; A4C3CED1482370FE CRC64;

Query Match      20.5%; Score 118.5; DB 1; Length 146;
Best Local Similarity 28.7%; Pred. No. 9e-06;
Matches 29; Conservative 16; Pident 33; Indels 23; Gaps 4;

QY   5 TFOKKHLLTNRDVCNNILSNLPHCKDKXKFNFIYSRDEPVAYIC--KGIIASKNV-LTT 60
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
Db    53 TMRRRLHLSP-----CKDTNFTHIGHNRHHNIALTCGDENGNPYGCGNLRIK 97

QY   61 SEFYLSDCNV---TSRPCKKYKLKSLNTFCVTENOAAPHV 97
    ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
Db    98 SPFOYTCKLHGSSPRPCCRIRATRGSRNIYVGENGCLPYH 138

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ID	RNP_PROGU	STANDARD:	PRT:	128 AA.
AC	P04059;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).			
GN	RNASE1 OR RNS1.			
OS	Proechimys guirae (Caetiguae).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys.			
OX	NCBI_TaxId=10163;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Pancreas;			
RX	MEDLINE=83000399; PubMed=7115727;			
RX	Beintema J.J., Krol G., Martena B.;			
RT	"The primary structures of pancreatic ribonucleases from African			
RT	porcupine and caetiguae, two hystriocomorph rodent species.";			
RL	Biochim. Biophys. Acta 705:102-110(1982).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Pancreas.			
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR: A00821; NRKS.			
DR	HSP, P00656; 1SRN.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF000074; rnasea; 1.			
DR	PRINTS: PR00794; RIBONUCLEASE.			
DR	Prodom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
FT	DISULFID 26	84		
FT	DISULFID 40	95		
FT	DISULFID 58	110		
FT	DISULFID 65	12		
FT	ACT_SITE 12	12		
FT	ACT_SITE 41	41		
FT	ACT_SITE 119	119		
FT	CAROHYD 34	34		
SEQ	SEQUENCE 128 AA; 14244 MW; 2DB58093JA9D3C936 CRC64;			
Query Match	20.3%; Score 117; DB 1; Length 128;			
Beet Local Similarity	29.1%; Pred. No. 1.1e-05;			
Matches	34; Conservative 19; Mismatches 36; Indels 28; Gaps 7			
Qy	6 FQKHL-----TNRDVCNNIL--STNLF--HCKDKNFIYSRPEVPAICKGIASIKV 57			
Db	8 FQRQIIDSQSGSSTNPNVNCNMKMSRMTQERCKRVNFFVHEPLADVQAVC----FQKRV 63			
Qy	58 -----LTSFYLSDCNVSR-----PCKYKLKSTNTFCTGQNG--APNPF 98			
Db	64 PCIKNQSNQCYSTSNMHTIDRLTNSNKFDPCLVYRTSQEKSIIIVACGPNPVVHF 120			

Search completed: January 22, 2004, 12:02:08  
Job time : 6.23221 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 (Search time 25.7079 Seconds  
(without alignments)  
1043.940 Million cell updates/sec

Title: US-09-622-613C-4  
Perfect score: 577  
Sequence: 1 QDWLTFOCKKLTNTRDVDCN.....TFCVTCENQAPVHPVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_Archea:\*  
2: SP\_Bacteria:\*  
3: SP\_Fungi:\*  
4: SP\_Human:\*  
5: SP\_Invertebrate:\*  
6: SP\_Mammal:\*  
7: SP\_mhc:\*  
8: SP\_Organelle:\*  
9: SP\_Phage:\*  
10: SP\_Plant:\*  
11: SP\_Rodent:\*  
12: SP\_Virus:\*  
13: SP\_Vertebrate:\*  
14: SP\_Unclassified:\*  
15: SP\_Virus:\*  
16: SP\_Bacteriophage:\*  
17: SP\_Archaeop:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	99.7	127	13	Q918V8
2	553	95.8	127	13	Q8UVX5
3	401.5	69.6	129	13	Q9DFY6
4	383	66.4	128	13	Q9DFY8
5	308	53.4	128	13	Q9DFY7
6	306	53.0	128	13	Q9DFY5
7	295	51.1	133	13	Q9DSMO
8	289	50.1	133	13	Q9PMR7
9	283	49.0	133	13	Q9PSL9
10	282	48.9	132	13	Q9PSL9
11	279	48.4	133	13	Q9PSM2
12	277	48.0	132	13	Q9PSM1
13	272.5	47.2	132	13	Q9DF78
14	156.5	27.1	169	13	Q9W738
15	128	22.2	157	11	Q9JKI9
16	127	22.0	157	11	Q9JKJ3

17	126	21.8	152	11	Q9JKI5	Q9JKI5 mus saxicol
18	126	21.8	157	11	Q9JKI4	Q9JKI4 meriones un
19	123.5	21.4	153	11	Q9JKI7	Q9JKI7 mus saxicol
20	123	21.3	157	11	Q9JKI1	Q9JKI1 meriones un
21	122	21.1	157	11	Q9JKI2	Q9JKI2 meriones un
22	120	20.8	154	11	Q9JKI8	Q9JKI8 mus saxicol
23	117.5	20.4	155	11	Q9JKI9	Q9JKI9 mus pahari
24	116.5	20.2	155	11	Q9JKI3	Q9JKI3 mus saxicol
25	114.5	19.8	155	11	Q9JKI8	Q9JKI8 mus pahari
26	113.5	19.7	132	6	Q9TV24	Q9TV24 galago moho
27	113.5	19.7	155	11	Q9JKI6	Q9JKI6 mus saxicol
28	112.5	19.5	132	6	Q9TV25	Q9TV25 eulemur ful
29	112.5	19.5	155	11	Q9JKI2	Q9JKI2 mus saxicol
30	112.5	19.5	155	11	Q9JKI4	Q9JKI4 mus saxicol
31	111.5	19.3	170	6	Q9BECL	Q9BECL tragulus ja
32	111	19.2	156	11	Q9JKG6	Q9JKG6 mus caroli
33	111	19.2	156	11	Q9JKG7	Q9JKG7 mus caroli
34	110.5	19.2	119	6	Q9TS06	Q9TS06 cercopithec
35	110.5	19.2	119	6	Q9TV32	Q9TV32 gorilla gor
36	110.5	19.2	147	6	Q9HZ00	Q9HZ00 pan troglod
37	110.5	19.2	155	11	Q9RI34	Q9RI34 ratius norv
38	110.5	19.2	155	11	Q9RI25	Q9RI25 mus musculu
39	110	19.1	156	11	Q9VHS0	Q9VHS0 mus musculu
40	110	19.1	156	11	Q9JKG7	Q9JKG7 mus caroli
41	109.5	19.0	119	6	Q9TV30	Q9TV30 saginus oe
42	109	18.9	124	6	Q9TSF2	Q9TSF2 bos taurus
43	109	18.9	156	11	Q9JKH4	Q9JKH4 mus caroli
44	109	18.9	156	11	Q9JKG9	Q9JKG9 mus caroli
45	109	18.9	156	11	Q9JKH5	Q9JKH5 mus caroli

## ALIGNMENTS

RESULT 1  
Q918V8 PRELIMINARY; PRT; 127 AA.

NC Q918V8; ID Q918V8; DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Onconase variant rap1a precursor.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CX Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
3' UTR of unusual length and structure."  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL: AF165133; AAF76935.1; --  
DR HSSP: P22069; IONC.  
DR InterPro: IPR001427; RNAsea.  
DR Pfam: PF00074; RNAsea; 1.  
DR ProDom: PD000535; RNAsea; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.7%; Score 575; DB 13; Length 127;  
Best Local Similarity 99.0%; Pred. No. 4.5e-57;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFOCKKLTNTRDVDCNIIISTULFCKDKNTFIYSRPEPVKAIKGIISKVLLTT 60  
DB 24 QDWLTFOCKKLTNTRDVDCNIIISTULFCKDKNTFIYSRPEPVKAIKGIISKVLLTT 83

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OY 61 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxId=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF332139; AAL54383.1;
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match
Best Local Similarity 95.8%; Score 553; DB 13; Length 127;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICKGIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242555; AAG31441.2;
DR HSSP: P22069; IONC.

RESULT 4
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAG31439.1;
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ CHAIN 1 23 POTENTIAL.
RC-RNASE2 RIBONUCLEASE.
FT SEQUENCE 128 AA; 14839 MW; 989719CF5205ECC CRC64;

Query Match
Best Local Similarity 66.4%; Score 383; DB 13; Length 128;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICKGIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 5
ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242555; AAG31441.2;
DR HSSP: P22069; IONC.
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DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match
Best Local Similarity 69.6%; Score 401.5; DB 13; Length 129;
Matches 70; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICKGIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 128

RESULT 4
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAG31439.1;
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ CHAIN 1 23 POTENTIAL.
RC-RNASE2 RIBONUCLEASE.
FT SEQUENCE 128 AA; 14839 MW; 989719CF5205ECC CRC64;

Query Match
Best Local Similarity 66.3%; Score 383; DB 13; Length 128;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICKGIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKTKKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 5
ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242555; AAG31441.2;
DR HSSP: P22069; IONC.
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ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR PRODOM; PD00035; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.4%; Score 308; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.4e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVDCNNILSTNLFHCKDKNTFYISRPVPYAKICKGIASKNVLTT 60
DB 24 QDWTFQKHLTDRKVCVDMKALFDCKKTNFYALPGRVYALCKNIKNDTNVLSR 83
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
DB 84 DAFLLPQCDRIKLPCHYLTSSTNTICITCVNQLPIHFAGVQSC 127

RESULT 6
ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR PRODOM; PD00035; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.4%; Score 308; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.4e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVDCNNILSTNLFHCKDKNTFYISRPVPYAKICKGIASKNVLTT 60
DB 24 QDWTFQKHLTDRKVCVDMKALFDCKKTNFYALPGRVYALCKNIKNDTNVLSR 83
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
DB 84 DAFLLPQCDRIKLPCHYLTSSTNTICITCVNQLPIHFAGVQSC 127

RESULT 7
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P1916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR PRODOM; PD00035; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.1%; Score 295; DB 13; Length 133;
Best Local Similarity 48.6%; Pred. No. 1.6e-25;
Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKHLTNRDVDCNNILSTNLFHCKDKNTFYISRPVPYAKICKGIASKNVLTT 56
DB 23 QNWATFOQKHITNTSSINCNTIMNNIYIVGGQCKGVNTFISSATYKALCTGVY -NMN 81
QY 57 VLTTSFYLSDC--NVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
DB 82 VLTSTRQLNLTCTRTSITPRCPYSSRTENNYICVGCENQAPVHFGVGHG 132

RESULT 8
ID Q9PMR7 PRELIMINARY; PRT; 133 AA.
AC Q9PMR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

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KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE8FD67D266C7C2 CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 9.1e-27;
Matches 55; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVDCNNILSTNLFHCKDKNTFYISRPVPYAKICKGIASKNVLTT 60
DB 24 QDWTFQKHLTDRKVCVDMKALFDCKKTNFYALPGRVYALCKNIKNDTNVLSR 83
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGHG 104
DB 84 DVFYLPQCNRRKLPCHYRLDGSNTNTICLTCKMKELPIHFAGVQKC 127

RESULT 9
ID Q9PMR7 PRELIMINARY; PRT; 133 AA.
AC Q9PMR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

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ID	NAME	SEQUENCE	SCORE	DB	LENGTH	GAPS
RL	J. Mol. Evol. 53:31-38(2001).					
DR	EMBL: AF351211; AAK30257.1; .					
DR	HSSP: P11916; 1BC4.					
DR	InterPro: IPR001427; RNaseA.					
DR	Pfam: PF00074; RNaseA; 1.					
DR	ProDom: PD000535; RNaseA; 1.					
DR	SMART: SM00092; RNase_Pc; 1.					
DR	PROSITE: PS00127; RNase_PANCREATIC; 1.					
KW	Signal.					
FT	SIGNAL					
SO	SEQUENCE	133 AA; 14590 MW; 8840B9A94FA5B943 CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				
		SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;				
		POTENTIAL.				
		1 22				

DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE RC-RnaaseII\_ribonuclease precursor.  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxId=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver.  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT "Purification and cloning of cytotoxic ribonucleases from Rana  
 catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver.  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF288642; AAC30414.2; -  
 DR HSSP; P11916; 1BC4.  
 DR InterPro; IPR001427; RNaaseA.  
 DR Pfam; PF00074; rnaaseA; 1.  
 DR ProDom; PD000535; RnaaseA; 1.  
 DR SMART; SM00092; RNaase\_Pc; 1.  
 DR PROSITE; PS00127; RNaase\_PANCREATIC; 1.  
 KW Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 132 RC-RnaaseII\_RIBONUCLEASE.  
 SO SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;  
  
 Query March 47.2%; Score 272.5; DB 13; Length 132;  
 Best Local Similarity 43.2%; Pred. No. 5,6e-23;  
 Matches 46; Conservative 20; Mismatches 36; Indels 7; Gaps 2;  
  
 QY 1 QDWLTFOKKGLTNRDVCNNILSTLNF---HCKDKNTFYSRPEPYKAIKGIASKN 56  
 Db 22 QNNAKFPEKRIITSTSSIDCMTINDKAIYVGGCKEKERNFIIISEDVNVKAIICGVSPPDK 81  
  
 QY 57 VLTSTSEYLYSDC---NVTSRPRCKYKLLKKSNTFCVCENAPAPHPGVGHC 104  
 Db 82 ELSTTSKLTCTIRDSTITPRCPYHSPDNKKICVCKEKLPPHFGIGKC 132  
  
 RESULT 14  
 Q9W738 PRELIMINARY; PRT; 169 AA.  
 AC Q9W738;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE FRL2 protein.  
 GN FRL2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxId=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96069863; PubMed=7585965;  
 RA Kinoshita N., Minshull J., Kirschner M.W.;  
 RT "The identification of two novel ligands of the FGF receptor by a  
 yeast screening method and their activity in Xenopus development.";  
 RL Cell 83:621-630(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kinoshita N., Kirschner M.W.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF159166; AAD41901.1; -  
 DR HSSP; P00656; IL5Q.  
 DR InterPro; IPR001427; RNaaseA.



DR Pfam: PF00074; rnaaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR ProSite: PS00127; RNase\_PANCREATIC; 1.  
SQ SEQUENCE 169 AA; 18851 MW; D969F3E43B3CE1B8 CRC64;

Query Match 27.1%; Score 156.5; DB 13; Length 169;  
Best Local Similarity 36.1%; Pred. No. 8.3e-10;  
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;

QY 6 FOKKHULTNT-RDVDCN-----NILSTNLFHCKDKNTFIY-SRPEPVKAICKGIASKNV 57  
DB 33 FWEKHIVVEGATNCNQTIKDKNIRPKN-NCKFRNTFIHDITNGKVKKEMCAGIVKSTFV 90  
QY 58 LTTSEFYLSDCNV---TSRP--CKYKLKXSTNTFCVTCENQAPVHPVG 100  
DB 91 ISKELLPLTDCLMGRTARPPNCAYNQTRTGVINITCENNYFVHPFAG 138

## RESULT 15

Q9JKI9 PRELIMINARY; PRT; 157 AA.  
AC Q9JKI9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Eosinophil-associated ribonuclease 44.  
GN EAR44.  
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Meriones.  
OK NCBI\_TaxID=10047;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20243759; PubMed=10758160;  
RA Zhang J., Dyer K.D., Rosenberg H.F.;  
RT "Evolution of the rodent eosinophil-associated ribonuclease gene  
family by rapid gene sorting and positive selection";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).  
DR EMBL: AF236394; AAF67694.1; -.  
DR HSSP: P10153; 1H12.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR ProSite: PS00127; RNase\_PANCREATIC; 1.  
SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;

Query Match 22.2%; Score 128; DB 11; Length 157;  
Best Local Similarity 30.3%; Pred. No. 1.3e-06;  
Matches 33; Conservative 21; Mismatches 35; Indels 20; Gaps 7;

QY 3 WLTFOKKHLNTRDVDCN-NILSTNLF-HCKDKNTFIYSRPEPV-----KAICKGI 52  
DB 36 WFTIQ--HISNTTICQNAAMLGNNVYTORCKDNLTFHLTRFANVNECVNRRTTCKN-- 91  
QY 53 ASKNVU-TSEFYLSDCNVTS-----RPCKYKLKXSTNTFCVTCENQAP 95  
DB 92 GRNCHDSRSKVSITDCNLITSPANYRQCRYORTRAKFRYRIACNNKTP 140

Search completed: January 22, 2004, 12:08:50  
Job time : 25.7079 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 : Search time 33.0337 Seconds  
(without alignment)  
504.524 Million cell updates/sec

Title: US-09-622-613C-8  
Perfect score: 580  
Sequence: 1 MODWTFCXKILTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.\*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.\*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.\*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	98.8	105	20	AA198869
2	571	98.4	105	20	AA198867
3	568	97.9	104	20	AA198866
4	566	97.6	104	20	AA198865
5	566	97.6	105	20	AA198871
6	566	97.6	127	20	AA198879
7	561	96.7	104	20	AA198870
8	546	94.1	104	18	AAW06544
9	546	94.1	105	18	AAW35123

10	546	94.1	105	20	AA193400	Recombinant frog O
11	546	94.1	355	18	AAW35125	R. pipiens recombi
12	546	94.1	358	18	AAW35130	R. pipiens recombi
13	544	93.8	104	18	AAW30301	Recombinant onc pr
14	544	93.8	104	22	AAW31666	Amino acid sequenc
15	544	93.8	104	23	ABG32650	Northern leopard f
16	544	93.8	112	18	AAW35118	R. pipiens recombi
17	544	93.8	251	18	AAW35134	R. pipiens recombi
18	544	93.8	254	18	AAW35135	R. pipiens recombi
19	544	93.8	355	18	AAW35129	R. pipiens recombi
20	544	93.8	355	18	AAW35133	R. pipiens recombi
21	544	93.8	366	18	AAW35132	R. pipiens recombi
22	544	93.8	379	18	AAW35126	R. pipiens recombi
23	543	93.6	104	18	AAW30302	Recombinant onc pr
24	541	93.3	104	12	AAW12344	Protein with activ
25	541	93.3	104	15	AAW47303	ONCONASE (pharmace
26	541	93.3	104	17	AAW00736	Protein derived fr
27	541	93.3	104	18	AAW06543	Antitumour protein
28	541	93.3	104	18	AAW14065	Onconase (RTM) pro
29	541	93.3	104	20	AAW33322	Frog onconase prot
30	541	93.3	104	20	AAW88233	Rana pipiens RNase
31	541	93.3	104	22	AAW31667	Amino acid sequenc
32	541	93.3	104	23	ABG31617	Northern leopard f
33	539	92.9	105	18	AAW35116	R. pipiens recombi
34	539	92.9	106	18	AAW35122	R. pipiens recombi
35	539	92.9	107	18	AAW35117	R. pipiens recombi
36	538	92.8	105	18	AAW35115	R. pipiens recombi
37	536	92.4	104	18	AAW18224	Antitumour genetic
38	535	92.2	358	18	AAW35127	R. pipiens recombi
39	535	92.2	365	18	AAW35131	R. pipiens recombi
40	516	89.0	107	18	AAW35120	R. pipiens recombi
41	483	83.3	360	18	AAW35128	R. pipiens recombi
42	471.5	81.3	111	18	AAW35121	R. pipiens recombi
43	433	74.7	83	20	AAW35119	R. pipiens clone R
44	433	74.7	83	20	AAW88234	Rana pipiens RNase
45	277	47.8	111	20	AAW33321	Frog lectin protei

ALIGNMENTS

RESULT 1	AA198869	AA198869 standard; Protein, 105 AA.
AC	AA198869;	
DT	25-JAN-2000	(first entry)
XX		
DE	Recombinant Met(-1) RapLRI Met23Jleu-(His)6 protein.	
XX		
KW	Recombinant Met(-1) Rana pipiens ribonuclease Met23Jleu-(His)6; RapLRI;	
KW	CD22; covalently bound; IL2 antibody; ligand binding moiety; RNase;	
KW	cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;	
KW	signal peptide; recombinant ribonuclease; cytotoxic fusion protein;	
KW	cancer; frog; autoimmune disease.	
OS	Rana pipiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 1	/note= "(His)6 histidine tag attached to N-terminal Met"
FT	Misc-difference 1	/note= "Met not found in wild type RapLRI"
FT	Misc-difference 24	/note= "wild type Met replaced with Leu"
XX		
PN	MO9950398-A2.	
XX		
XX	07-OCT-1999.	
PD		
XX		
PF	26-MAR-1999;	99WO-US06641.



XX WPI: 1999-610847/52.  
 DR N-PSDB; AA208125.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PS treating cancers, viral infections or autoimmune diseases -  
 PS  
 PS Claim 34; Page 56; 71pp; English.  
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)  
 CC protein with Met31Leu. Carboxy terminal end of recombinant RapLR1 has a  
 CC covalently bound ligand binding moiety, which can be a L12 antibody  
 CC directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases.  
 CC  
 SQ Sequence 104 AA;  
 Query Match 97.9%; Score 568; DB 20; Length 104;  
 Best Local Similarity 99.0%; Pred. No. 1.3e-60;  
 Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFTSRPEPVAKICKGIASKNVLT 61  
 DB 1 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFTSRPEPVAKICKGIASKNVLT 60  
 OY 62 SEFYISDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGHC 105  
 DB 61 SEFYISDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGHC 104  
 RESULT 4  
 AAY28865  
 ID AAY28865 standard; Protein; 104 AA.  
 AC AAY28865;  
 XX  
 XX 25-JAN-2000 (first entry)  
 DT  
 XX  
 XX Rana pipiens liver ribonuclease (RaplR1).  
 DE  
 XX  
 XX Rana pipiens liver ribonuclease; RapLR1; covalently bound; L12 antibody;  
 KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;  
 KW human chorionic gonadotropin; hCG; recombinant ribonuclease; RNase;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.  
 XX  
 OS Rana pipiens.  
 PN WO9950398-A2.  
 XX  
 XX 07-OCT-1999.  
 PD  
 XX 26-MAR-1999; 99WO-US06641.  
 PF  
 XX 27-MAR-1998; 98US-0079751.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Newton DL, Rybak SM;  
 PI  
 XX WPI: 1999-610847/52.  
 DR N-PSDB; AA208124.  
 XX  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases -  
 PS  
 PS Claim 1; Page 55; 71pp; English.

CC The present sequence is Rana pipiens liver ribonuclease (RaplR1)  
 CC protein. Carboxy terminal end of RapLR1 has a covalently bound  
 CC ligand binding moiety, which can be a L12 antibody directed against  
 CC CD22 on cancerous B cells or human chorionic gonadotropin (hCG)  
 CC effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can  
 CC be expressed in bacteria without an N-terminal methionine due to the  
 CC presence of a signal peptide that is cleaved by bacteria. The soluble  
 CC expression of ribonuclease allows the proteins to be fused in-frame with  
 CC ligand binding moieties to form cytotoxic fusion proteins. They can be  
 CC used for treatment of cancer and autoimmune diseases.  
 CC  
 SQ Sequence 104 AA;  
 Query Match 97.6%; Score 566; DB 20; Length 104;  
 Best Local Similarity 98.1%; Pred. No. 2.2e-60;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFTSRPEPVAKICKGIASKNVLT 61  
 DB 1 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFTSRPEPVAKICKGIASKNVLT 60  
 OY 62 SEFYISDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGHC 105  
 DB 61 SEFYISDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGHC 104  
 RESULT 5  
 AAY28871  
 ID AAY28871 standard; Protein; 105 AA.  
 AC AAY28871;  
 XX  
 XX 25-JAN-2000 (first entry)  
 DT  
 XX  
 XX Recombinant Met(-1) RapLR1 GlnSer amino acid sequence.  
 DE  
 XX  
 KW Recombinant Met(-1) Rana pipiens ribonuclease GlnSer; RapLR1; CD22;  
 KW covalently bound; L12 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
 KW autoimmune disease; RNase.  
 XX  
 OS Rana pipiens.  
 PN WO9950398-A2.  
 XX  
 XX 07-OCT-1999.  
 PD  
 XX 26-MAR-1999; 99WO-US06641.  
 PF  
 XX 27-MAR-1998; 98US-0079751.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Newton DL, Rybak SM;  
 PI  
 XX WPI: 1999-610847/52.  
 DR N-PSDB; AA208129.  
 XX  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases -  
 PS  
 PS Claim 34; Page 61; 71pp; English.  
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)  
 CC protein with Met at position 1 and GlnSer. Carboxy terminal end of

recombinant RAPLRI has a covalently bound ligand binding moiety, which can be a IL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases.

Sequence 105 AA;

Query Match 97.6%; Score 566; DB 20; Length 105;

Best Local Similarity 97.1%; Pred. No. 2.2e-60; Mismatches 0; Gaps 0;

Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MODMLTFQKKHLTNTRDVCNNILSTNLFPHCKDKNTFTISRPEPVAKIGIIASKNVLT 60

1 MEDMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFTISRPEPVAKIGIIASKNVLT 60

61 TSEFYISDCNVTSRPCKRYLKXSTTFTCYTCENQAPVHFVGVGHC 105

61 TSEFYISDCNVTSRPCKRYLKXSTTFTCYTCENQAPVHFVGVGHC 105

61 TSEFYISDCNVTSRPCKRYLKXSTTFTCYTCENQAPVHFVGVGHC 105

RESULT 6  
AA28879 standard; Protein; 127 AA.

AA28879 standard; Protein; 127 AA.

AA28879;

25-JAN-2000 (first entry)

Rana pipiens Clone 5a1b ribonuclease.

Rana pipiens ribonuclease Clone 5a1b; RAPLRI; covalently bound; RNase; IL2 antibody; ligand binding moiety; CD22; cancerous B cell; oncogene; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein; autoimmune disease.

Rana pipiens.

Location/Qualifiers

1..23 /label= Signal\_peptide

24..127 /note= "putative"

/label= Rana\_pipiens\_Clone\_5a1b\_ribonuclease

MO9950398-A2.

07-OCT-1999.

26-MAR-1999; 99WO-US06641.

27-MAR-1998; 98US-0079751.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL, Rybak SM;

WPI; 1999-610847/52.

N-PSDB; AA208136.

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases -

Disclosure; Page 69; 71pp; English.

The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RAPLRI). It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncogene (RTM) at amino acid

residues 11, 20, 85 and 103. Carboxy terminal end of RAPLRI has a covalently bound ligand binding moiety, which can be a IL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases.

Sequence 127 AA;

Query Match 97.6%; Score 566; DB 20; Length 127;

Best Local Similarity 98.1%; Pred. No. 2.8e-60; Mismatches 1; Indels 0; Gaps 0;

2 QDMLTFQKKHLTNTRDVCNNILSTNLFPHCKDKNTFTISRPEPVAKIGIIASKNVLT 61

24 QDMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFTISRPEPVAKIGIIASKNVLT 83

62 SEFYISDCNVTSRPCKRYLKXSTTFTCYTCENQAPVHFVGVGHC 105

62 SEFYISDCNVTSRPCKRYLKXSTTFTCYTCENQAPVHFVGVGHC 105

84 SEFYISDCNVTSRPCKRYLKXSTTFTCYTCENQAPVHFVGVGHC 127

RESULT 7  
AA28870 standard; Protein; 104 AA.

AA28870 standard; Protein; 104 AA.

AA28870;

25-JAN-2000 (first entry)

Recombinant RAPLRI Glniser amino acid sequence.

Recombinant Rana pipiens ribonuclease; RAPLRI Glniser; covalently bound; IL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase; autoimmune disease.

Rana pipiens.

Location/Qualifiers

1 /note= "Wild type Gln replaced with Ser"

MO9950398-A2.

07-OCT-1999.

26-MAR-1999; 99WO-US06641.

27-MAR-1998; 98US-0079751.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL, Rybak SM;

WPI; 1999-610847/52.

N-PSDB; AA208128.

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases -

Claim 34; Page 60; 71pp; English.

The present sequence is a recombinant Rana pipiens ribonuclease (RAPLRI) protein with Glniser. Carboxy terminal end of recombinant RAPLRI has a covalently bound ligand binding moiety, which can be a IL2 antibody directed against CD22 on cancerous B cells or human chorionic



```

XX AC AAY39400;
XX DT 01-DEC-1999 (first entry)
XX DE Recombinant frog Oncnase.
XX KM Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
XX OS Rana pipiens.
XX PN MO9946389-A1.
XX PD 16-SEP-1999.
XX PF 11-MAR-1999; 99MO-US04252.
XX PR 11-MAR-1998; 98US-0077557.
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Goldenberg DM, Hansen H, Leung S;
XX DR WPI: 1999-551416/46.
XX DR N-PSDB; AAZ19767.
XX PT A new recombinant Oncnase used to treat, e.g. colon cancer -
XX PS Example 1; Fig 1; 42pp; English.
XX
CC This sequence represents recombinant frog Oncnase. Oncnase has
CC ribonuclease and anti-tumour activity. The cDNA was produced via PCR
CC (using primers AAZ19768-219769) of two synthetic DNAs whose sequences
CC encoded most of the N-terminal or the C-terminal amino acids of mature
CC Oncnase. The two PCR products generated encoded either the N-terminal
CC 54 amino acids (minus the initial methionine) or the C-terminal 51 amino
CC acids, and were ligated in frame at an NruI site. The cDNA was then
CC subcloned into a vector e.g., pBluescript, where the AUG initiation
CC codon was ligated to the cDNA. After expression in E. coli, the
CC recombinant protein was purified. The initial N-formyl methionine was
CC cleaved off and the now N-terminal glutamate residue cyclised to form an
CC N-terminal pyroglutamate. The pyroglutamate residue forms part of the
CC phosphate binding pocket of Oncnase and is essential for both
CC ribonuclease and anti-tumour activity. Oncnase is a 12 kD ribonuclease
CC which causes cell death as a result of potent inhibition of protein
CC synthesis by a mechanism involving inactivation of cellular RNA. It is
CC not inhibited by mammalian placental ribonuclease inhibitor, which may
CC explain its enhanced cytotoxicity relative to mammalian enzymes. It has
CC anti-tumour activity against a variety of solid tumours e.g., colon or
CC pancreatic cancers, and can be used alone or in combination with other
CC anti-cancer agents such as tamoxifen. When used as an anti-tumour agent,
CC Oncnase can be conjugated to a marker which targets it to a specific
CC cell type.
CC
SQ Sequence 105 AA;
Query Match 94.1%; Score 546; DB 20; Length 105;
Best Local Similarity 93.3%; Pred. No. 5.7e-58;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 MODMLTFQKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
DB 1 MQDWLTFQKKHINTKDVCDDNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
QY 61 TSEFYISDCNVTSPCKYKXKSTITFCVTCENQAPVHPFGVGHG 105
DB 61 TSEFYISDCNVTSPCKYKXKSTITFCVTCENQAPVHPFGVGHG 105
RESULT 11
AAW35125
ID AAW35125 standard; Protein; 355 AA.

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```

AC AAW35125;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 1.
XX KM RNase A; ribonuclease; cytotoxic; oncnase; nOnc; immunofusion;
XX OS Rana pipiens.
XX PN MO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97MO-US02588.
XX PR 21-FEB-1996; 96US-0011800.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Boque L, Newton DL, Rybak SM, Wlodawer A;
XX DR WPI: 1997-435168/40.
XX DR N-PSDB; AAT94963.
XX PT Ribonuclease molecules based on native Oncnase - used for killing
XX PS cells, particularly tumour cells
XX PS Disclosure; Page 67; 90pp; English.
XX
CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (fOnc) which are modifications of the RNase Oncnase (rOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and
CC also lower immunogenicity in humans.
CC
SQ Sequence 355 AA;
Query Match 94.1%; Score 546; DB 18; Length 355;
Best Local Similarity 93.3%; Pred. No. 2.8e-57;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 MODMLTFQKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
DB 251 MEDMLTFQKKHINTKDVCDDNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 310
QY 61 TSEFYISDCNVTSPCKYKXKSTITFCVTCENQAPVHPFGVGHG 105
DB 311 TSEFYISDCNVTSPCKYKXKSTITFCVTCENQAPVHPFGVGHG 355
RESULT 12
AAW35130
ID AAW35130 standard; Protein; 358 AA.
XX
AC AAW35130;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 6.
XX KM RNase A; ribonuclease; cytotoxic; oncnase; nOnc; immunofusion;
XX KW tumour cell growth; frog.
XX

```

OS	Rana pipiens.
OS	Synthetic.
XX	
PN	WO9731116-A2.
XX	
PD	28-AUG-1997.
XX	
PF	19-FEB-1997; 97WO-US02588.
XX	
XX	21-FEB-1996; 96US-0011800.
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Bogue L, Newton DL, Rybak SM, Wlodawer A;
XX	
DR	WPI; 1997-435168/40.
N-PSDB; AAT94968.	
XX	
PT	Ribonuclease molecules based on native Onconase - used for killing
XX	cells, particularly tumour cells
PS	Disclosure; Page 72; 90pp; English.
CC	
XX	
CC	Sequences AAM35125 to AAM35135 represent recombinant fusion proteins
CC	(rOnc) which are modifications of the RNase Onconase (RTM) (nonc). Such
CC	novel ribonuclease molecules are highly cytotoxic and can be used alone
CC	or to form chemical conjugates or to target recombinant immunofusions.
CC	They are used particularly for decreasing tumour cell growth. They can
CC	also be used for cell separation in vitro by selectively killing unwanted
CC	types of cells, e.g. in bone marrow prior to transplantation into a
CC	patient undergoing marrow ablation by radiation, or for killing leukaemia
CC	cells or T-cells that would cause graft versus host disease. The toxins
CC	can also be used to selectively kill unwanted cells in culture. The new
CC	ribonucleases have increased cytotoxic activity compared to nonc and
CC	also lower immunogenicity in humans.
XX	
SQ	Sequence 358 AA:
Query Match	94.1%; Score 546; DB 18; Length 358;
Best Local Similarity	93.3%; Pred. No. 2.8e-57;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0	
Oy	1 MODWLTPQKGLTNRDVCNNILSTLPHCKDKNTFIYSRPEPYAKICKGIASGNVLT 60
Dd	1 MEDWLTFOKKHITNTRDVDCDNIMSTNLPHCKDKNTFIYSRPEPYAKICKGIASGNVLT 60
Oy	61 TSEFYLSDCNVTSRPCKYKLKKSITIIFCYTCENQAPVHVGVGCHC 105
Dd	61 TSEFYLSDCNVTSRPCKYKLKKSITNKFCVTCENQAPVHFVGVSIC 105
RESULT 13	
AAM30301	
AAM30301 standard; protein; 104 AA.	
AC	AAM30301;
XX	
DT	09-JUN-1998 (first entry)
DE	Recombinant onc protein.
KW	onc; oncnase; ribonuclease; frog; antitumour; pancreatic cancer;
human immunodeficiency virus type-1; HIV1; replication.	
Rana pipiens.	
MO9738112-Al.	
16-OCT-1997.	
04-APR-1997; 97WO-US05675.	
04-APR-1996; 96US-0626288.	

XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA	
XX	
PI	Ardelt W, Boix E, Vasandani VM, Wu YN, Youle RJ;
XX	
DR	WPI; 1997-512725/47.
XX	
PT	Recombinant Onc protein with glutamine residue at position 1 -
PT	useful as antitumour and antiviral agent, also as cell culture
PT	selection agent
XX	
PS	Claim 1; Page 28; 35pp; English.
XX	
CC	This sequence represents a recombinant Onc protein comprising a 104 amino
CC	acid sequence having Gln at position 1. Onc, a ribonuclease from Rana
CC	pipiens oocytes, is known as an antitumour agent (e.g. for treating
CC	pancreatic cancer) and inhibitor of human immunodeficiency virus type-1
CC	replication. It can be used therapeutically or as a cell-culture
CC	selection agent, e.g. to identify gene therapy compositions able to
CC	inhibit tumour growth.
XX	
SQ	Sequence 104 AA;
XX	
Query Match	93.8%; Score 544; DB 18; Length 104;
Beat Local Similarity	94.2%; Pred. No. 9.9e-58;
Matches	98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX	
OY	2 QDWLTPOKXHLTNRDVCNNILSTNLPHCKDKKTFIYSREPVKAIICKGIASKVLT 61
DB	1 QDWLTFQKHITNTRDVCDDIMWSTNLFHCKDKKTFIYSREPVKAIICKGIASKVLT 60
XX	
OY	62 SEFYLSDCNVTSRPCKYKLLKKSITTFCTGCENQAPVHFVGCHC 105
DB	61 SEFYLSDCNVTSRPCKYKLLKKSITTFCTGCENQAPVHFVGSC 104
XX	
RESULT 14	
ID	AAB31666
XX	AAB31666 standard; protein: 104 AA.
XX	
AC	AAB31666;
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Amino acid sequence of a frog ribonuclease protein.
XX	
KW	Frog; ribonuclease; ranpirinase; RNase.
XX	
OS	Rana pipiens.
XX	
XX	
FH	Key
FT	Modified-site 1 Location/Qualifiers
FT	/note= "this Gln is autocyclised to pyroglutamic acid"
XX	
FN	US6175003-B1.
XX	
PD	16-JAN-2001.
XX	
PF	10-SEP-1999; 99US-0394268.
XX	
PR	10-SEP-1999; 99US-0394268.
XX	
PA	(ALFA-) ALFACELL CORP.
XX	
PI	Saxena SK.
XX	
DR	WPI; 2001-167808/17.
XX	
XX	New nucleic acids encoding a ribonuclease (RNase), useful for the
XX	precise targeting of RNase to a predetermined cell receptor
XX	
XX	Claim 1; Columns 5-6; 7pp; English.





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:30 : Search time 12.5843 Seconds  
(without alignments)  
353.031 Million cell updates/sec

Title: US-09-622-613C-8

Perfect score: 580

Sequence: 1 MODULFQKXHLTNRDVC.....TECVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	94.1	104	1	US-08-467-955-2
2	546	94.1	105	3	US-08-875-811-39
3	546	94.1	355	3	US-08-875-811-41
4	546	94.1	358	3	US-08-875-811-51
5	544	93.8	104	4	US-09-394-268-1
6	544	93.8	104	4	US-09-687-748-1
7	544	93.8	112	3	US-08-875-811-32
8	544	93.8	129	3	US-08-875-811-63
9	544	93.8	251	3	US-08-875-811-59
10	544	93.8	354	3	US-08-875-811-61
11	544	93.8	355	3	US-08-875-811-49
12	544	93.8	355	3	US-08-875-811-57
13	544	93.8	355	3	US-08-875-811-64
14	544	93.8	366	3	US-08-875-811-55
15	544	93.8	379	3	US-08-875-811-43
16	541	93.3	104	1	US-08-283-971-1
17	541	93.3	104	1	US-07-921-619-1
18	541	93.3	104	1	US-08-467-955-1
19	541	93.3	104	2	US-08-891-848-13
20	541	93.3	104	3	US-09-394-268-2
21	541	93.3	104	4	US-09-687-748-2
22	539	92.9	104	4	US-08-875-811-1
23	539	92.9	104	4	US-09-071-672-1
24	539	92.9	105	3	US-08-875-811-26
25	539	92.9	105	3	US-08-875-811-28
26	539	92.9	107	3	US-08-875-811-30
27	538	92.8	105	3	US-08-875-811-24

28	535	92.2	358	3	US-08-875-811-45	Sequence 45, Appl
29	535	92.2	365	3	US-08-875-811-53	Sequence 53, Appl
30	516	89.0	107	3	US-08-875-811-20	Sequence 20, Appl
31	483	83.3	360	3	US-08-875-811-47	Sequence 47, Appl
32	471.5	81.3	111	3	US-08-875-811-22	Sequence 22, Appl
33	433	74.7	83	3	US-08-875-811-2	Sequence 2, Appl
34	433	74.7	83	4	US-09-071-672-3	Sequence 3, Appl
35	277	47.8	111	3	US-08-891-848-12	Sequence 12, Appl
36	277	47.8	111	3	US-08-875-811-8	Sequence 8, Appl
37	205.5	35.4	114	3	US-09-223-118-4	Sequence 4, Appl
38	193.5	33.4	114	3	US-09-223-118-2	Sequence 2, Appl
39	192.5	33.2	114	3	US-09-223-118-1	Sequence 1, Appl
40	190.5	32.8	114	3	US-09-223-118-3	Sequence 3, Appl
41	152.5	26.3	169	1	US-08-441-629-2	Sequence 2, Appl
42	152.5	26.3	169	3	US-08-776-207-2	Sequence 2, Appl
43	152.5	26.3	169	4	US-09-507-773-2	Sequence 2, Appl
44	152.5	26.3	169	5	PCT-US95-09172-2	Sequence 2, Appl
45	143	24.7	28	3	US-08-875-811-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1

US-08-467-955-2

Sequence 2, Application US/08467955

Patent No. 572805

GENERAL INFORMATION:

APPLICANT: Ardelt Ph.D, Wojciech J.

TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: Mark H. Jay, P.A.

STREET: P.O. Box E

CITY: Short Hills

STATE: New Jersey

COUNTRY: USA

ZIP: 07078-0383

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,955

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/178,118

FILING DATE: 06-APR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/436,141

FILING DATE: 13-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,332

FILING DATE: 03-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,970

FILING DATE: 01-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jay, Mark H.

REGISTRATION NUMBER: 27507

REFERENCE/DOCKET NUMBER: 5007 US

TELEPHONE: 201-912-9066

TELEFAX: 201-912-0442

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana pipiens  
DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-2

Query Match 94.1%; Score 546; DB 1; Length 104;  
Best Local Similarity 94.2%; Pred. No. 8.7e-60;  
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKXHLNTRDVCNNILSTNLFHCKDKXTFYISRPPEVYAKICKGIIASKVLT 61  
Db 1 EDWLTFOKXHLNTRDVCNNIMSTNLFHCKDKXTFYISRPPEVYAKICKGIIASKVLT 60  
QY 62 TSEFYLSDCNVTSRPCKYKUKKSTITFCVTCENQAPVHFVGHC 105  
Db 61 TSEFYLSDCNVTSRPCKYKUKKSTITFCVTCENQAPVHFVGHC 104

RESULT 2  
US-08-875-811-39  
Sequence 39; Application US/08875811  
Patent No. 6045793

GENERAL INFORMATION:  
APPLICANT: Rydak, Sueanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Lulu  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-39

Query Match 94.1%; Score 546; DB 3; Length 105;  
Best Local Similarity 93.3%; Pred. No. 8.8e-60;  
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MODWLTFOKXHLNTRDVCNNILSTNLFHCKDKXTFYISRPPEVYAKICKGIIASKVLT 60  
Db 1 MEDWLTFOKXHLNTRDVCNNIMSTNLFHCKDKXTFYISRPPEVYAKICKGIIASKVLT 60  
QY 61 TSEFYLSDCNVTSRPCKYKUKKSTITFCVTCENQAPVHFVGHC 105  
Db 61 TSEFYLSDCNVTSRPCKYKUKKSTITFCVTCENQAPVHFVGHC 105

RESULT 3  
US-08-875-811-41  
Sequence 41; Application US/08875811  
Patent No. 6045793

GENERAL INFORMATION:  
APPLICANT: Rydak, Sueanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Lulu  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-41

Query Match 94.1%; Score 546; DB 3; Length 355;  
Best Local Similarity 93.3%; Pred. No. 4.4e-59;  
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MODWLTFOKXHLNTRDVCNNILSTNLFHCKDKXTFYISRPPEVYAKICKGIIASKVLT 60  
Db 251 MEDWLTFOKXHLNTRDVCNNIMSTNLFHCKDKXTFYISRPPEVYAKICKGIIASKVLT 310

QY 61 TSEFYLSDCNVTSRPCKYKUKKSTITFCVTCENQAPVHFVGHC 105  
Db 311 TSEFYLSDCNVTSRPCKYKUKKSTITFCVTCENQAPVHFVGHC 355

RESULT 4  
US-08-875-811-51

Sequence 51, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Mlodaver, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-51

Query Match 94.1%; Score 546; DB 3; Length 358;  
Best Local Similarity 93.3%; Pred. No. 4.4e-59;  
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MODWLTFQKHLITNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLT 60  
DB 1 MEDWLTFQKHLITNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLT 60

QY 61 TSEFYSDCNVTSRPPCKYKLLKSKSTTFCTVCENQAPVHPVGVGHC 105  
DB 61 TSEFYSDCNVTSRPPCKYKLLKSKSTNKFCTVCENQAPVHPVGVGSC 105

RESULT 5  
US-09-394-268-1  
Sequence 1, Application US/09394268  
Patent No. 6175003  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shalendra K  
APPLICANT: Mlodaver, Alexander  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF  
FILE REFERENCE: 5013  
CURRENT APPLICATION NUMBER: US/09/394,268  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1

LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-394-268-1

Query Match 93.8%; Score 544; DB 3; Length 104;  
Best Local Similarity 94.2%; Pred. No. 1.5e-59;  
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLITNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLT 61  
DB 1 QDWLTFQKHLITNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLT 60

QY 62 SEFYLSDCNVTSRPPCKYKLLKSKSTTFCTVCENQAPVHPVGVGHC 105  
DB 61 SEFYLSDCNVTSRPPCKYKLLKSKSTNKFCTVCENQAPVHPVGVGSC 104

RESULT 6  
US-09-687-748-1  
Sequence 1, Application US/09687748  
Patent No. 6423515  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shalendra K  
FILE REFERENCE: 5013 US 01  
CURRENT APPLICATION NUMBER: US/09/687,748  
CURRENT FILING DATE: 2000-10-14  
PRIOR APPLICATION NUMBER: 09/394,268  
PRIOR FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-687-748-1

Query Match 93.8%; Score 544; DB 4; Length 104;  
Best Local Similarity 94.2%; Pred. No. 1.5e-59;  
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLITNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLT 61  
DB 1 QDWLTFQKHLITNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKVLT 60

QY 62 SEFYLSDCNVTSRPPCKYKLLKSKSTTFCTVCENQAPVHPVGVGHC 105  
DB 61 SEFYLSDCNVTSRPPCKYKLLKSKSTNKFCTVCENQAPVHPVGVGSC 104

RESULT 7  
US-08-875-811-32  
Sequence 32, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Mlodaver, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-32

Query Match 93.8%; Score 544; DB 3; Length 112;  
Best Local Similarity 93.3%; Pred. No. 1,76-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MODLTFQKXHLTRDVCNNILSTNLFHCKDKNTFYISRPVKAICKGIASKNVLT 60  
DB 8 MSDMLTQKXHLTRDVCNNILSTNLFHCKDKNTFYISRPVKAICKGIASKNVLT 67  
QY 61 TSEFYLSDCNVTSPCKYKLLKSKTITFCVTCENQAPVHFVGVC 105  
DB 68 TSEFYLSDCNVTSPCKYKLLKSKTITFCVTCENQAPVHFVGVC 112

RESULT 8  
US-08-875-811-63  
Sequence 63, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-63

Query Match 93.8%; Score 544; DB 3; Length 129;  
Best Local Similarity 94.2%; Pred. No. 26-59;  
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKXHLTRDVCNNILSTNLFHCKDKNTFYISRPVKAICKGIASKNVLT 61  
DB 26 QDWLTFQKXHLTRDVCNNILSTNLFHCKDKNTFYISRPVKAICKGIASKNVLT 85  
QY 62 SEFYLSDCNVTSPCKYKLLKSKTITFCVTCENQAPVHFVGVC 105  
DB 86 SEFYLSDCNVTSPCKYKLLKSKTITFCVTCENQAPVHFVGVC 129

RESULT 9  
US-08-875-811-59  
Sequence 59, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-875-811-59

Query Match 93.8%; Score 544; DB 3; Length 251;  
Best Local Similarity 93.3%; Pred. No. 4.9e-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60  
Db 147 MSDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 206

Qy 61 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105  
Db 207 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 251

RESULT 10

US-08-875-811-61  
; Sequence 61, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Bogue, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,800  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-244100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-875-811-61

Query Match 93.8%; Score 544; DB 3; Length 254;  
Best Local Similarity 93.3%; Pred. No. 5e-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60  
Db 1 MSDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60

Qy 61 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105  
Db 207 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 251

Db 61 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105

RESULT 11  
US-08-875-811-49  
; Sequence 49, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Bogue, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,800  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-244100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-875-811-49

Query Match 93.8%; Score 544; DB 3; Length 355;  
Best Local Similarity 93.3%; Pred. No. 7.7e-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60  
Db 251 MSDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 310

Qy 61 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105  
Db 311 TSEFYLSDCNVTSRCKYKLLKSKSTTFCVTCENQAPVHFVGVC 355

RESULT 12  
US-08-875-811-57  
; Sequence 57, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Bogue, Lluís  
; APPLICANT: Wlodawer, Alexander

Qy 1 MODWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60  
Db 1 MSDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60

TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-57

Query Match 93.8%; Score 544; DB 3; Length 355;  
Best Local Similarity 93.3%; Pred. No. 7.7e-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MODWLTFOKKHLTNTDVCNNLTSTNLFPHCKDKNTFTYSRPPVKAICKGIITASKVLT 60  
DB 1 MSDWLTFQKKHITNTDVCNNLTSTNLFPHCKDKNTFTYSRPPVKAICKGIITASKVLT 60

QY 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105  
DB 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGSC 105

RESULT 13  
US-08-875-811-64  
Sequence 64, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..355  
OTHER INFORMATION: /note="EGFB[Met-(-1)]Seronc"  
US-08-875-811-64

Query Match 93.8%; Score 544; DB 3; Length 355;  
Best Local Similarity 93.3%; Pred. No. 7.7e-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MODWLTFOKKHLTNTDVCNNLTSTNLFPHCKDKNTFTYSRPPVKAICKGIITASKVLT 60  
DB 251 MSDWLTFQKKHITNTDVCNNLTSTNLFPHCKDKNTFTYSRPPVKAICKGIITASKVLT 310

QY 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105  
DB 311 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGSC 355

RESULT 14  
US-08-875-811-55  
Sequence 55, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Luis  
APPLICANT: Mlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-55

Query Match 93.8%; Score 544; DB 3; Length 366;  
Best Local Similarity 93.3%; Pred. No. 8.1e-59;  
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MODLTFQKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60  
DB 262 MSDMLTFQKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 321  
OY 61 TSEFYLSDCNVTSRPECKYKLLKSTITFCVTCENQAPVHFVGHC 105  
DB 322 TSEFYLSDCNVTSRPECKYKLLKSTINKFCVTCENQAPVHFVGVC 366

## RESULT 15

US-08-875-811-43  
Sequence 43, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Bogue, Louis  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 379 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-43

Query Match 93.8%; Score 544; DB 3; Length 379;  
Best Local Similarity 94.2%; Pred. No. 8.4e-59;  
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 ODMLTFQKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 61  
DB 26 ODMLTFQKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 85  
OY 62 SEFYLSDCNVTSRPECKYKLLKSTITFCVTCENQAPVHFVGHC 105  
DB 86 SEFYLSDCNVTSRPECKYKLLKSTINKFCVTCENQAPVHFVGVC 129

Search completed: January 22, 2004, 12:10:06  
Job time: 12.5843 secs



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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 : Search time 24.9719 Seconds  
(without alignments)  
869.271 Million cell updates/sec

Title: US-09-622-613C-8  
Perfect score: 580  
Sequence: 1 MODWLTFOKKHLTNTRDVC.....TFCVTGENDQAPVHFGVGHIC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	99.0	105	US-09-948-391A-8	Sequence 8, Appli
2	574	99.0	111	US-09-948-391A-9	Sequence 9, Appli
3	573	98.8	111	US-09-961-400-9	Sequence 9, Appli
4	571	98.4	105	US-09-948-391A-6	Sequence 6, Appli
5	571	98.4	105	US-09-961-400-6	Sequence 2, Appli
6	566	97.6	104	US-09-961-400-2	Sequence 2, Appli
7	566	97.6	105	US-09-948-391A-13	Sequence 13, Appli
8	566	97.6	105	US-09-961-400-13	Sequence 13, Appli
9	566	97.6	127	US-09-948-391A-28	Sequence 28, Appli
10	566	97.6	127	US-09-961-400-28	Sequence 28, Appli
11	563	97.1	105	US-09-961-400-8	Sequence 8, Appli
12	562	96.9	104	US-09-948-391A-4	Sequence 4, Appli
13	562	96.9	104	US-09-961-400-4	Sequence 4, Appli
14	561	96.7	104	US-09-948-391A-11	Sequence 11, Appli
15	561	96.7	104	US-09-961-400-11	Sequence 11, Appli

16	557	96.0	104	US-09-948-391A-2	Sequence 2, Appli
17	549	94.7	105	US-10-153-882-2	Sequence 2, Appli
18	539	92.9	104	US-09-986-119-1	Sequence 1, Appli
19	539	92.9	104	US-09-918-887-1	Sequence 1, Appli
20	433	74.7	83	US-09-986-119-3	Sequence 3, Appli
21	433	74.7	83	US-09-918-887-3	Sequence 3, Appli
22	275.5	47.5	111	US-09-948-391A-21	Sequence 21, Appli
23	275.5	47.5	111	US-09-961-400-21	Sequence 21, Appli
24	275.5	47.5	117	US-09-948-391A-22	Sequence 22, Appli
25	275.5	47.5	117	US-09-961-400-22	Sequence 22, Appli
26	274.5	47.3	111	US-09-961-400-17	Sequence 17, Appli
27	270.5	46.6	110	US-09-961-400-19	Sequence 19, Appli
28	269.5	46.5	110	US-09-948-391A-15	Sequence 15, Appli
29	269.5	46.5	110	US-09-961-400-15	Sequence 15, Appli
30	269.5	46.5	111	US-09-948-391A-26	Sequence 26, Appli
31	269.5	46.5	111	US-09-961-400-26	Sequence 26, Appli
32	268.5	46.3	111	US-09-948-391A-17	Sequence 17, Appli
33	264.5	45.6	110	US-09-948-391A-19	Sequence 19, Appli
34	264.5	45.6	110	US-09-948-391A-24	Sequence 24, Appli
35	264.5	45.6	110	US-09-961-400-24	Sequence 24, Appli
36	152.5	26.3	169	US-10-016-447-2	Sequence 2, Appli
37	143	24.7	119	US-10-074-978A-139	Sequence 139, App
38	122.5	21.1	124	US-10-016-447-5	Sequence 5, Appli
39	109	18.8	147	US-09-286-240-6	Sequence 6, Appli
40	109	18.8	147	US-09-863-777-2	Sequence 2, Appli
41	109	18.8	147	US-09-731-872-254	Sequence 254, App
42	109	18.8	147	US-09-876-997-254	Sequence 254, App
43	106	18.3	124	US-09-981-286A-8	Sequence 8, Appli
44	100.5	17.3	99	US-10-074-978A-141	Sequence 141, App
45	98.5	17.0	89	US-10-074-978A-143	Sequence 143, App

## ALIGNMENTS

RESULT 1  
US-09-948-391A-8  
; Sequence 8, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Diane L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948.391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens  
; OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu  
; OTHER INFORMATION: substitution (recombinant Met(-1) RapiRi Met23Leu)  
US-09-948-391A-8

Query Match 99.0% Score 574; DB 11; Length 105;  
Best Local Similarity 99.0% Pred No. 3e-56; 1; Indels 0; Gaps 0;  
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MODWLTFOKKHLTNTRDVCNNILSTNLFFCKDKNTFTYSRPPYKAIKGIASKNVLT 60  
|||||

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Db      1  MODLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Qy      61  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      61  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105

RESULT 2
US-09-948-391A-9
; Sequence 9, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with (His)6 tag, Met at position 7
; OTHER INFORMATION: and Met30Leu substitution (recombinant Met(-1))
; OTHER INFORMATION: RapLR1 Met23Leu-(His)6)
US-09-948-391A-9

Query Match          99.0%; Score 574; DB 11; Length 111;
Best Local Similarity 99.0%; Pred. No. 3.2e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MODLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      7  MODLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 66
Qy      61  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      67  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 111

RESULT 3
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-9

Query Match          98.4%; Score 573; DB 11; Length 111;
Best Local Similarity 99.0%; Pred. No. 4.2e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MODLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      7  MODLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 66
Qy      61  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      67  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 111

RESULT 4
US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
; OTHER INFORMATION: Met(-1) RapLR1)
US-09-948-391A-6

Query Match          98.4%; Score 571; DB 11; Length 105;
Best Local Similarity 98.1%; Pred. No. 6.7e-58;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MODLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      1  MODLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Qy      61  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      61  TSEFYSLDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105

RESULT 5
US-09-961-400-6
; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
```

```

; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-6

Query Match          98.4%; Score 571; DB 11; Length 105;
Best Local Similarity 98.1%; Pred. No. 6.7e-58;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
DB 1 MDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 6
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-2

Query Match          97.6%; Score 566; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 2.5e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
DB 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 62 SEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
DB 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
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US-09-948-391A-13
; Sequence 13, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser
; OTHER INFORMATION: substitution (recombinant Met(-1) RnPLR1 Q1S)
US-09-948-391A-13

Query Match          97.6%; Score 566; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 2.5e-57;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
DB 1 MSDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 8
US-09-961-400-13
; Sequence 13, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-13

Query Match          97.6%; Score 566; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 2.5e-57;
```

Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MQDMLTFQKKHLTNRDVDCNNILSTNLFHCKDKNTFISRPEPYAKICKGIASKVLT 600  
| | | | | : | | | | | | | | | | | | | | | | | | | | | |  
DB 1 MSDMLTFQKKHLTNRDVDCNNIMSTNLFHCKDKNTFISRPEPYAKICKGIASKVLT 600

QY	Db
61 TSEFYSLDCNVTSRPCCKYLLKKSTITFCVTCENQAPVHFGVGH	61 TSEFYSLDCNVTSRPCCKYLLKKSTITFCVTCENQAPVHFGVGH
105	105

RESULT 9  
US-09-948-391A-28

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; Publication No. US20030027311A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Rybak, Susanna M.

```

APPLICANT: as represented by The Secretary of the Department of Health and Human Services

FILE REFERENCE: 015280-343110US  
CURRENT APPLICATION NUMBER: US/09/948,391A  
CURRENT FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
 ; PRIOR FILING DATE: 1999-03-26

```

; PRIOR FILING DATE: 2000-08-17
;
; NUMBER OF SEQ ID NOS: 43
;
; SOFTWARE: PatentIn Ver. 2.0

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```

; LENGTH: 127
;
; TYPE: PRT
; ORGANISM: Rana pipiens
;

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; OTHER INFORMATION: Rana pipiens ribonuclease (RafLRI) clone 5a1b cDNA
;
; OTHER INFORMATION: insert
US-09-948-391A-28

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Query March	97.6%	Score 566, DB 11,	length 127,
Best Local Similarity	98.1%	Pred. No. 3.1e-57,	
Matches 102; Conservative	1;	Mismatches	0; Gaps 0;

**Qy**      2 QDMLTFQKHEL TNTRDVDCNNILSTNLNLFHCKDKATFIYSRPEPVAAICKGIIASKVLT 61  
         ||||| : |||||  
**Dd**      24 QDMLTFQKHL TNTRDVDCNNIMSTNLNLFHCKDKATFIYSRPEPVAAICKGIIASKVLT 83

```

Qy      62 SEFYLSDCNVTSRPCKYKYLKSTITFCVTCENQAPVHFGVGH 105
         |||||
Db      84 SEFYLSDCNVTSRPCKYKYLKSTNTFCVTCENQAPVHFGVGH 127

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RESULT 10  
US-09-961-400-28

Publication No. US20030124131A1  
GENERAL INFORMATION:  
APPLICANT: RYBAK, SUSANNA M.

APPLICANT: NEWTON, DIANNE L.  
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
TITLE OF INVENTION: CELLS

```

; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613

```

; PRIOR APPLICATION NUMBER: PCT/US99/06641  
 ;  
 ; PRIOR FILING DATE: 1999-03-26  
 ;  
 ; PRIOR APPLICATION NUMBER: 60/079,751

PRIOR FILING DATE: 1998-03-26  
NUMBER OF SEQ. IN NOS. 43

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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 127  
NAME DATE
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ORGANISM: Rana pipiens  
US-09-961-400-28

Matches	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
102;								

Db 24 QDWLTFQKGLHNTRDVDCNNIMSTNLFHCKDKNTFIYSRBPVKAIC

Db 84 SEFYLSDCNVTSRPCKYKLLKKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 11  
US-09-961-400-8  
; Sequence 8, Application US/09961400

APPLICANT: RYBAK, SUSANNA M.  
APPLICANT: GOLDENBERG, DAVID M.

;; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
;; TITLE OF INVENTION: CELLS  
;; FILE REFERENCE: 018733/1059

```

; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17

```

; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079,751  
 ; PRIOR FILING DATE: 1998-03-26

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 105

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! ORGANISM: Rana pipiens  
US-09-961-400-8

Best Local Similarity 97.1%; Pred. No. 5.5e-57;  
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps

1 MQDWLTFQKQGLTNTROYDCNNILSTNLFCCKDKNTFIYSRPEPKALCKGIIASKNVL 6

Db 61 TFEFLSDCNATSRPCKYKTKKSTNTFCVTCEHQAPVHFVGVGHC 105

RESULT 12  
US-09-948-391A-4  
: Sequence 4, Application US/09948391A

```

; GENERAL INFORMATION:
;
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.

```

APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Recombinant Anti-Tumor Rhase

```
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
/ OTHER INFORMATION: ribonuclease with Met23Ileu substitution
/ OTHER INFORMATION: (recombinant RapLRI Met23Ileu)
US-09-948-391A-4
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Query Match          96.9%; Score 562; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 7,1e-57;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 ODMLTFOKKHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 61
Db 1 ODMLTFOKKHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 60

Qy 62 SEFYISDCNVTSRPCKYKLLKKSSTITFCVTCENQAPVHFVGCHC 105
Db 61 FEFYISDCNVTSRPCKYKLLKKSSTITFCVTCENQAPVHFVGCHC 104
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RESULT 13
US-09-961-400-4
/ Sequence 4, Application US/09961400
/ Publication No. US20030124131A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Rana pipiens
US-09-961-400-4
```

```
Query Match          96.9%; Score 562; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 7,1e-57;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ODMLTFOKKHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 61
Db 1 ODMLTFOKKHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 60

Qy 62 SEFYISDCNVTSRPCKYKLLKKSSTITFCVTCENQAPVHFVGCHC 105
Db 61 FEFYISDCNVTSRPCKYKLLKKSSTITFCVTCENQAPVHFVGCHC 104
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RESULT 14
US-09-948-391A-11
/ Sequence 11, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
/ OTHER INFORMATION: ribonuclease with Gln1ser substitution
/ OTHER INFORMATION: (recombinant RapLRI Q1S)
US-09-948-391A-11
```

```
Query Match          96.7%; Score 561; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 9,3e-57;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 DMLTFOKKHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 62
Db 2 DMLTFOKKHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 61

Qy 63 EFYISDCNVTSRPCKYKLLKKSSTITFCVTCENQAPVHFVGCHC 105
Db 62 EFYISDCNVTSRPCKYKLLKKSSTITFCVTCENQAPVHFVGCHC 104
```

```
RESULT 15
US-09-961-400-11
/ Sequence 11, Application US/09961400
/ Publication No. US20030124131A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Rana pipiens
US-09-961-400-11
```

Query Match 96.7%; Score 561; DB 11; Length 104;  
 Best Local Similarity 98.1%; Pred. No. 9.3e-57;  
 Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	3	DMLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAI	CKGIIASKNVLTTS	62
Db	2	DMLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAI	CKGIIASKNVLTTS	61
QY	63	EFYLSDCNVTSRPCKYKLLKSTIITFCVTCENQAPVHFGVGHG		105
Db	62	EFYLSDCNVTSRPCKYKLLKSTIITFCVTCENQAPVHFGVGHG		104

Search completed: January 22, 2004, 12:12:25  
 Job time : 24.9719 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 (Search time 11.7978 Seconds  
(without alignments)  
855.901 Million cell updates/sec

Title: US-09-622-613C-8

Perfect score: 580

Sequence: 1 MODMLTFQKXHLTNTRDVC.....TFCVTCENQAPVHFGVGHG 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_76: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	541	93.3	104	2	A39035	ribonuclease-relat
2	277	47.8	111	2	A27121	ribonuclease-relat
3	273.5	47.2	111	1	JX0120	ribonuclease-relat
4	257.5	44.4	111	2	JX0085	pancreatic ribonuc
5	143	24.7	119	2	S41111	pancreatic ribonuc
6	125	21.6	124	1	NRU1	pancreatic ribonuc
7	122	21.0	125	1	A32474	angiotensin [valida
8	120	20.7	128	1	NRU1	pancreatic ribonuc
9	119	20.5	124	1	NRU1	pancreatic ribonuc
10	115.5	19.9	145	1	A35332	angiotensin precurs
11	114	19.7	128	1	NRU1	angiotensin precurs
12	113	19.5	125	1	B43825	angiotensin - rabbi
13	113	19.5	128	1	NRU1	angiotensin - rabbi
14	111	19.1	124	1	NRU1	pancreatic ribonuc
15	110	19.0	128	1	NRU1	pancreatic ribonuc
16	109	18.8	147	1	NRU1	pancreatic ribonuc
17	108	18.6	124	1	NRU1	pancreatic ribonuc
18	106.5	18.4	123	1	A43825	angiotensin - pig
19	106	18.3	124	1	NRU1	pancreatic ribonuc
20	106	18.3	124	1	NRU1	pancreatic ribonuc
21	106	18.3	150	1	NRU1	pancreatic ribonuc
22	105.5	18.2	147	2	I52489	ribonuclease 4 (EC
23	105	18.1	124	2	S08549	ribonuclease 4 (EC
24	105	18.1	128	1	NRU1	pancreatic ribonuc
25	105	18.1	128	1	NRU1	pancreatic ribonuc
26	105	18.1	167	2	S20066	pancreatic ribonuc
27	104.5	18.0	155	2	JC6159	eosinophil-associat
28	103	17.8	124	1	NRU1	pancreatic ribonuc
29	103	17.8	124	1	NRU1	pancreatic ribonuc

30	103	17.8	124	1	NRGPA	pancreatic ribonuc
31	103	17.8	124	2	S07141	pancreatic ribonuc
32	102	17.6	124	1	NRMB	pancreatic ribonuc
33	102	17.6	124	1	NRGN	pancreatic ribonuc
34	102	17.6	124	1	NRGM	pancreatic ribonuc
35	101	17.4	124	1	NRGF	pancreatic ribonuc
36	101	17.4	156	2	JC6160	eosinophil-associat
37	99	17.1	124	1	NREDO	pancreatic ribonuc
38	99	17.1	124	1	NREKN	pancreatic ribonuc
39	99	17.1	124	1	NRCHM	pancreatic ribonuc
40	99	17.1	124	1	NRCHB	pancreatic ribonuc
41	99	17.1	128	1	NRCH2	pancreatic ribonuc
42	98	16.9	124	1	NRHY	pancreatic ribonuc
43	97	16.7	124	1	NRDER	pancreatic ribonuc
44	97	16.7	124	1	NRDEN	pancreatic ribonuc
45	96	16.6	124	1	NRDEF	pancreatic ribonuc

#### ALIGNMENTS

##### RESULT 1

A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C/Species: Rana pipiens (northern leopard frog)

C/Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 30-Jun-1993

C/Accession: A39035

R/Ardelet, W.; Mikuleki, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A/Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl

A/Reference number: A39035; MUID:91093131; PMID:1985896

A/Accession: A39035

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-104 <ARD>

C/Superfamily: pancreatic ribonuclease

Query Match 93.3% Score 541; DB 2; Length 104;  
Best Local Similarity 93.3%; Pred. No. 2.4e-48;  
Matches 97; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKXHLTNTRDVCNNILSTNLFKCKDKNTFIYSRPEPVKAIKGIISKNVLT 61  
DB 1 EDWLTFOKXHLTNTRDVCDDNINSTNLFKCKDKNTFIYSRPEPVKAIKGIISKNVLT 60  
QY 62 SEFYLSDCNVTSPCKYKXKSTTTCVTCENQAPVHFGVGHG 105  
DB 61 SEFYLSDCNVTSPCKYKXKSTTTCVTCENQAPVHFGVGHG 104

##### RESULT 2

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C/Species: Rana catesbeiana (bullfrog)

C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993

C/Accession: A27121

R/Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kanauchi, H.; Takeyanagi

Biochemistry 26, 2189-2194, 1987

A/Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A/Reference number: A27121; MUID:87299649; PMID:3304421

A/Accession: A27121

A/Molecule type: protein

A/Residues: 1-111 <DTT>

C/Superfamily: pancreatic ribonuclease

C/Keywords: lectin

Query Match 47.8% Score 277; DB 2; Length 111;  
Best Local Similarity 46.8%; Pred. No. 2.7e-21;  
Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 2 QDWLTFQKXHLTNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVKAIKGIISKNV 57  
DB 1 ENMATFOOQHILNTINPTINDNNIYIVGGQCKRNVTFIISATYVACTGVI-NMN 59





R:Bond, M.D.; Stridom, D.J.  
 Biochemistry 28, 6110-6113, 1989  
 A:Title: Amino acid sequence of bovine angiotensin.  
 A:Reference number: A52474; MUID:89375344; PMID:275757  
 A:Accession: A32474  
 A:Molecule type: protein  
 A:Residues: 1-125 <BON>  
 A:Experimental source: plasma  
 R:Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.  
 FEBS Lett. 241, 41-45, 1988  
 A:Title: The complete amino acid sequence of bovine milk angiotensin.  
 A:Reference number: S02001; MUID:89065101; PMID:3197838  
 A:Accession: S02001  
 A:Molecule type: protein  
 A:Residues: 1-125 <MAE>  
 A:Experimental source: milk  
 R:Racharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
 submitted to the Brookhaven Protein Data Bank, January 1995  
 A:Reference number: A65065; PDB:1AC1  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125  
 R:Racharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995  
 A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.  
 A:Reference number: A58315; MUID:95224057; PMID:7708754  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms  
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
 submitted to the Brookhaven Protein Data Bank, April 1996  
 A:Reference number: A65709; PDB:1G10  
 A:Contents: annotation; conformation by (1)H-NMR, residues 1-125  
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
 Biochemistry 35, 8670-8680, 1996  
 A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy.  
 A:Reference number: A58821; MUID:96280645; PMID:8688423  
 A:Contents: annotation; conformation by (1)H-NMR  
 R:Reisdorf, C.; Aberger, D.; Bontems, F.; Lallemand, J.Y.; Decotignies, J.P.; Spik, G.  
 Eur. J. Biochem. 224, 811-822, 1994  
 A:Title: Proton resonance assignments and secondary structure of bovine angiotensin.  
 A:Reference number: S48212; MUID:95010071; PMID:7925406  
 A:Contents: annotation; conformation by (1)H-NMR  
 A:Function:  
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: angiogenesis; hydrolysis; nucleic acid degradation  
 F:60-68/Region: receptor binding #status predicted  
 F:14,41,115/Active site: His, Lys, His #status predicted  
 F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 21.0%; Score 122; DB 1; Length 125;  
 Best Local Similarity 33.0%; Pred. No. 2.2e-05;  
 Matches 32; Conservative 15; Mismatches 32; Indels 18; Gaps 5;

Oy 17 DVDGNILSTNLF--HCKDKNTFYSPPEPKAICKGIASKN-----VLTSEFYL 66  
 Db 24 DEYFNMMKNKRLTRPCDRNTFTFGNKNDDKAICE---DRNGQPYRGDIRKISSEFQI 79  
 Oy 67 SDC---NWTSR-PCKYTKKSTFTFCVTCENQDAVHF 99  
 Db 80 TICCHKGGSSRPCKRYGATSDSRVIVGCEGLFVHF 116

RESULT 8  
 NRCU  
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Myocastor coypus (nutria, coypu)  
 C:Date: 24-Apr-1994 #sequence\_rev15ion 30-Sep-1988 #text\_change 31-Mar-2000  
 C:Accession: A00822  
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
 Biochim. Biophys. Acta 453, 400-409, 1976  
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
 A:Reference number: A90612; MUID:77065676; PMID:999896  
 A:Accession: A00822  
 A:Molecule type: protein

```

A:Residues: -128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.7%; Score 120; DB 1; Length 128;
Best Local Similarity 29.1%; Pred. No. 3.5e-05;
Matches 34; Conservative 19; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKHLL-----TNRDVDNNIL-STNLF---HCKDKNFYISRPBPVKAICKGIASKNV 58
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 8 FERQHMDSRGSPSTNPVNCNEMMKSRNNTOGRCKRPVTFVHEPLADVAVC---FQKNV 63
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||

QY 59 L-----TTSEFYLDSCNVTSRP---CKYKLKSTTFPCVTCENQ--APVHF 99
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 64 LCKNGQNCVGSNSNMHMTDCRVTSNSDYPNCSIRTSQEEKSIYVACGNGVYPVHF 120
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 9
NRMK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N:Alternate names: RNase A, RNase A
C:Species: Balenoptera acutorostrata (minke whale, lesser torqual)
C:Date: 24-Apr-1984 #sequence, revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser torqual) pancreatic ribo-
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.5%; Score 119; DB 1; Length 124;
Best Local Similarity 27.7%; Pred. No. 4.3e-05;
Matches 33; Conservative 16; Mismatches 42; Indels 28; Gaps 6;

QY 5 LTFQKHLLTTRDVD-----CNILSTNLF---HCKDKNFYISRPBPVKAICKGIASK 56
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 6 MKFQRMDSGNSGNNPNYCNQMMRRKKTQGRCKRPVTFVHESLEDYAVC-----SQK 61
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||

QY 57 NVL-----TTSEFYLDSCNVTSRP---CKYKLKSTTFPCVTCENQ--APVHF 99
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 62 NVLCKNGRTNCYESNSTMHTIDCRQTSKYPNCAYTSQEKHIIVACGNPVYPVHF 120
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 10
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence, revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91050023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BDN>
A:Cross-references: GB:U2516; NID:g726325; PIDN:AAA91366.1; PID:g726326
A:Genetics:
A:Functions: #status absent

```

A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid  
F:1..24/Domain: signal sequence #status predicted <SIG>  
F:25..145/Product: angiosenin #status predicted <MAT>  
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:37,64/Active site: His, Lys, His #status predicted  
F:50..104,63..115,81..130/Disulfide bonds: #status predicted

Query Match	19.9%	Score 115.5	DB 1	Length 145
Best Local Similarity	35.5%	Pred No. 0.00012		
Matches 27	Conservative 11	Mismatches 31	Indels 7	Gaps 3

```
OY      31 CKDKNTFIYSRPEPVKAIC--KGILSKNV-LTSEFYLSDCVTS----RPCKYLKKS 83
        ||| |||| : |||| : :: :: :: | ||| :
DB      63 CKDVNFIHGKNKSNIKAI CGANGSPYRENLRLMSKSPQVTTCHTGSGPRPPCQYRASAG 122
```

```
QY      84 TITFCVTCEAQPVHF 99
          : ||| |||
DB     123 FRHVVIACENGLPVHF 138
```

RESULT 11  
NRKS  
pancreatic ribonuclease (EC 3.1.27.5) - Casiragu

C/Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 30-Sep-1993  
C/Accession: A00821  
R/Beintema, J.J.; Knol, G.; Martena, B.

A:Title: The primary structures of pancreatic ribonucleases from African porcupine and  
A:Reference number: A90644; MUID:83000399; PMID:7115727  
;Accession: A00821

A;Residues: 1-128<BEI>  
A;Note: residues 67-78 were positioned primarily by homology with other ribonucleases  
C;Superfamily: pancreatic ribonuclease

F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match	19.7%	Score 114	DB 1	Length 128
Best Local Similarity	29.1%	Pred. No. 0.00015		
Matches 34	Conservative 19	Mismatches 36	Indels 28	Gaps 7

```

0y      7 FOKKHL-----TNTRDVDCNNIL-STNLF--HCKDKNTFLYSRPEPKAICGIIASKNV 58
      ||::||      :||::||      ||::||      ||::||      ||
Db      8 FQKHIDSSGSPSTNPNYCNAMKSRNMQERCKRVNTFVHEPLADYQAVC----FOKNV 63

```

```

Qy 59 -----LTTSEFYLSDCNVTSR-----PCKYKLKSTITPCVTCENQ--APVHF 99
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 64 PCKNGOSNCYISTSNMHIITDCILUTSNKFPDCLYRTSQEKSIIIVACEGNPYVPHF 120

```

RESULT 12  
B43825

C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S29833; B43825

Bloembergen, W.G., Selye, H., Picot, D., Lelievre, L.D.  
 Blochm. Biophys. Acta 1162, 177-186, 1993  
 Article: Characterization and sequencing of rabbit, pig and mouse angiotensins: disarmed  
 A:Reference number: S29833; MUID:93192291; PMID:844812

A/Accession: Q27052  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-125 <BON>

C:Superfamily: pancreatic ribonuclease  
 C:Keywords: pyroglutamic acid  
 F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 PDBCC: submitted to the Protein Sequence Database, DECEMBER 1992

Query Match	113	Score	113	DB 1	length	125
Best Local Similarity	31.24	Pred.	No.	0	00018	
Matches	24	Conservative	13	Mismatches	32	Indels
					8	Gaps
						3

[illegible]

Qy 83 STITFCVTCEHQAPVHF 99  
          : : ||| |||  
Db 99 GSRNIVIACENGLPVHF 115

RESULT 13  
NRCPB

N:Alternate names: RName IB  
C:Species: *Cavia porcellus* (guinea pig)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000

R. van den Berg, A.; van den Herde-Himmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J. A. *Eur. J. Biochem.* **75**, 91-100, 1977

A;Accession: A00826  
A;Molecule type: protein  
A;Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
E:12,41,119/Active site: His, Lys, His #status predicted

Query Match 19.5%; Score 113; DB 1; Length 128;

by	5	LIFEOKHJ-----	TNTRDVDCNNIL---	STNLFHCKDKNTFYISR	PEPVKAIKGI	IAS	55
		33;	Conservative	22;	Mismatches	35;	
					Indels	30;	Gaps
							77

Db 6 MKFQHQHDEGSPSNSSNY--CNVMMIRRMNQGRCKPNTFVHESLADQAVC-----FQ 60

Oy 56 KNVL-----TTFSEFYSLDCNNTSRP----CKYLKKSTITFCVTENQ--APVHF 99

Db 61 KNTLCKNGQTNCTSYSRMRITDCVTSSSKFPNCSYRMSQAOKSIIVACEDDPYVPVHF 120

pancreatic ribonuclease (EC 3.1.27.5) - *Chinchilla brevicaudata* (tentative sequence)  
N:Alternate names: RNase 1; RNase A

CisSpecies: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata  
CDate: 24-Apr-1984 #sequence 30-Sep-1988 #text\_change 31-Mar-2000  
CAccession: A00820  
C: van den Bergh A.: van den Hende-Timmer l.: Beintema J.J.

**Biochim. Biophys. Acta** 453, 400-409, 1976  
**A1>Title:** Isolation, properties and primary structure of coypu and chinchilla pancreatic A90612; MUID:77065676; PMID:999896  
**A1.Reference number:** A90612; MUID:77065676; PMID:999896  
**A1.Accession number:** 000820

A;Molecule type: protein  
A;Residues: 1-124 <VAN>  
A;Note: a second component of chinchilla ribonuclease has 32-Asp  
C;Superfamily: pancreatic ribonuclease

**Keywords** glycoprotein; hydrolase; nucleic acid digestion; pancreas  
**C12,41,119/Active site:** His, Lys, His #status predicted  
**F2,6-84,40-95,58-110,65-72/Disulfide bonds:** #status predicted  
**F34/Binding site:** carbohydrate (Aen) [covalent] #status experimental

Query Match	19.1%	Score 111	DB 1	Length 124
Best Local Similarity	26.1%	Pred. No. 0.00029		
Matches	11	Conservative	20	Mismatches 40
		Indels	38	Gaps 5

Matches	31;	Conservative	20;	Mismatches	40;	Indels	28;	Gaps	6;
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[illegible]

## RESULT 15

pancreatic ribonuclease (EC 3.1.27.5) - capybara  
N:Alternate names: RNase 1, RNase A  
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 29-Oct-1999  
C:Accession: A00824  
R:Beintema, J.J.; Neuteboom, B.  
J. Mol. Evol. 19, 145-152, 1983  
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequence with that of the pancreatic ribonuclease  
A:Reference number: A92957; MUID:87036770; PMID:6571219  
A:Accession: A00824  
A:Molecule type: protein  
A:Residues: 1-128 <BE1>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: hydrolase; nucleic acid digestion; pancreas  
E:12-41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match	Score	DB 1	Length
19.0%	110	128	

Matches 31; Conservative 22; Mismatches 42; Indels 20; Gaps 6;

QY 5 LTFQKGL-----TNRDVCNNILSTNLF-----HCDKDTFIYSRPEPAVIC-KIILS 55  
 Db 6 MKFQHQVDSGSSSSNANYCNEMVRRKQTDQRCKPVPVFHEPLADVQAVCFQGNVPC 65  
 QY 56 KYNULT-----SEFYLSDDCVNTR-----PKYLLKKSITIFCYTCGNO--APHP 99  
 Db 66 KNGQNTCYOSYSMAHITDCRVTSNSKFPDOSTFTTQAKSIVACGSLVYPVHF 120

Search completed: January 22, 2004, 12:03:21  
Job time : 11.7978 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: January 22, 2004, 12:01:20 ; Search time 6.29213 Seconds  
(without alignments)  
784.758 Million cell updates/sec

Title: US-09-622-613C-8  
Perfect score: 580  
Sequence: 1 MODWLTFQKHLJNTRDYDC.....TFCVTCENQAPVHFGVGHG 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	544	93.8	104	1	RN30_RANPI
2	280	48.3	111	1	RNPO_RANCA
3	273.5	47.2	111	1	LECS_RANCA
4	257.5	44.4	111	1	RNPL_RANCA
5	143	24.7	119	1	RNPI_IGUG
6	127.5	22.0	145	1	ANGR_MOUSE
7	127.5	22.0	145	1	ANGI_MOUSE
8	125	21.6	124	1	RNP_GALMU
9	122	21.0	148	1	ANGI_BOVIN
10	120	20.7	128	1	RNP_MYOCO
11	119	20.5	124	1	RNP_BALAC
12	118.5	20.4	146	1	ANGI_MACMG
13	115.5	19.9	145	1	ANGI_MOUSE
14	115.5	19.9	146	1	ANGI_PAPHA
15	114	19.7	128	1	RNP_PROGU
16	113	19.5	125	1	ANGI_RABIT
17	113	19.5	128	1	RNPB_CAVPO
18	111	19.1	124	1	RNP_CHIBR
19	110	19.0	128	1	RNP_HYDHY
20	110	19.0	146	1	ANGI_MIORA
21	110	19.0	156	1	ECR3_MOUSE
22	109	18.8	147	1	ANGI_HUMAN
23	109	18.8	147	1	ANGI_PANTR
24	108	18.6	124	1	RNP_HIPAM
25	106.5	18.4	123	1	ANGI_PIG
26	106	18.3	124	1	RNP_PIG
27	106	18.3	150	1	RNP_BOVIN
28	106	18.3	156	1	RNP_MYOGI
29	105.5	18.2	147	1	RNS4_HUMAN
30	105	18.1	128	1	RNP_HYSCR
31	105	18.1	128	1	RNP_HYSCR
32	105	18.1	146	1	ANGI_SAGOE
33	105	18.1	167	1	RNBR_BOVIN

34	104.5	18.0	150	1	RNSE_SAIISC	O46529 saimiri sci
35	104.5	18.0	155	1	ECPI_MOUSE	P97426 mus musculu
36	104	17.9	141	1	RNBR_GIRCA	O29542 giraffa cam
37	104	17.9	146	1	ANGI_SAIISC	O8w60 saimiri sci
38	104	17.9	151	1	RNBR_AXIPR	PR7350 axis porcin
39	103	17.8	123	1	ANG2_BOVIN	P08029 bos taurus
40	103	17.8	124	1	RNPA_CAVPO	P06678 cavia porce
41	103	17.8	124	1	RNP_AEPME	P07847 aepyceros m
42	103	17.8	124	1	RNP_ANTAM	P06668 antilocapra
43	103	17.8	124	1	RNP_SHEEP	P00651 ovis aries
44	102	17.6	124	1	RNP_BUBBU	P00657 bubalus bub
45	102	17.6	124	1	RNP_CAMDR	P00670 camelus dro

## ALIGNMENTS

RESULT 1  
ID RN30\_RANPI STANDARD; PRT; 104 AA.  
AC P22069;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE P-30 protein (EC 3.1.27.-) (Onconase).  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN (1)  
RP SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=9109311; PubMed=1985896;  
RA Ardeli W., Mikulski S.M., Shogen K.;  
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";  
RL J. Biol. Chem. 266:245-251(1991).  
RN (2)  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE=93066156; PubMed=1438177;  
RA Mosimann S.C., Ardeli W., Mikulski S.M., Shogen K.,  
RA James M.N.G.;  
RT "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";  
RL Proteins 14:392-400(1992).  
RN (3)  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
RX MEDLINE=94166079; PubMed=8120892;  
RA Mosimann S.C., Ardeli W., James M.N.G.;  
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";  
RL J. Mol. Biol. 236:1141-1153(1994).  
CC - FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.  
CC - DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).  
CC - SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR PDB; 1ONC; 31-JAN-94.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SMO0092; RNaseA; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; 3D-structure;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 10  
FT ACT\_SITE 10 10  
FT ACT\_SITE 31 31  
FT ACT\_SITE 97 97  
FT DISULFD 19 68  
FT DISULFD 30 75  
FT PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 48 90  
 FT DISULFID 87 104  
 FT HELIX 3 10  
 FT STRAND 11 12  
 FT STRAND 19 22  
 FT HELIX 23 24  
 FT TURN 26 30  
 FT STRAND 33 38  
 FT STRAND 33 38  
 FT HELIX 41 45  
 FT HELIX 46 48  
 FT TURN 49 50  
 FT STRAND 55 58  
 FT STRAND 63 70  
 FT TURN 74 75  
 FT STRAND 77 84  
 FT STRAND 86 91  
 FT TURN 92 93  
 FT STRAND 94 101  
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 93.8%; Score 544; DB 1; Length 104;  
 Best Local Similarity 94.2%; Pred. No. 1.3e-52;  
 Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPKAICKGIASKNVLTT 61  
 Db 1 QDWLTQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPKAICKGIASKNVLTT 60  
 QY 62 SEFYLSDCNVTSPKCKYKLLKKSITTFCTGCENQAPVHFGVGHG 105  
 Db 61 SEFYLSDCNVTSPKCKYKLLKKSITTFCTGCENQAPVHFGVGHG 104

## RESULT 2

ID RNPO RANCA STANDARD; PRT; 111 AA.  
 AC P11916;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (sialic acid-binding  
 lectin) (SBL-C).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Egg;  
 RX MEDLINE=87296649; PubMed=3304421;  
 RA Titani K., Takio K., Kuwada M., Nitte K., Sakakibara F., Kawauchi H.,  
 RA Takayanagi G., Hakomori S.,  
 RT "Amino acid sequence of sialic acid binding lectin from frog (Rana  
 catesbeiana) eggs.";  
 RL Biochemistry 26:2189-2194(1987).  
 RN [2]  
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.  
 RX MEDLINE=82220613; PubMed=1373237;  
 RA Liao Y.-D.;  
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana  
 catesbeiana (bullfrog) oocytes.";  
 RL Nucleic Acids Res. 20:1371-1377(1992).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC TISSUE=Egg;  
 RX MEDLINE=83192604; PubMed=8448385;  
 RA Nitte K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,  
 RA Takayanagi Y., Hakomori S., Titani K.;  
 RT "Ribonuclease activity of sialic acid-binding lectin from Rana  
 catesbeiana eggs.";  
 RL Glycobiology 3:37-45(1993).  
 RN [4]  
 RP STRUCTURE BY NMR.

RX MEDLINE=98437383; PubMed=9761686;  
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
 RT "The solution structure of a cytotoxic ribonuclease from the oocytes  
 of Rana catesbeiana (bullfrog).";  
 RL J. Mol. Biol. 283:231-244(1998).  
 CC -1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine  
 as substrates, and prefers the former. The S-lectins in frog eggs  
 may be involved in the fertilization and development of the frog  
 embryo. This lectin agglutinates various animal cells, including  
 normal lymphocytes, erythrocytes, and fibroblasts of animal and  
 human origin.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PIR; A27121; A27121.  
 DR PDB; 1BC4; 28-OCT-98.  
 DR PDB; 1M07; 21-JAN-03.  
 DR InterPro: IPR001427; RNASEA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR ProDom; PD000355; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KM Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;  
 KM Pyroliadone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 FT HELIX 3 10  
 FT HELIX 19 23  
 FT TURN 26 27  
 FT STRAND 37 41  
 FT STRAND 45 51  
 FT TURN 52 52  
 FT STRAND 57 62  
 FT STRAND 68 73  
 FT STRAND 83 88  
 FT STRAND 92 97  
 FT TURN 98 99  
 FT STRAND 100 107  
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;  
 Query Match 48.3%; Score 280; DB 1; Length 111;  
 Best Local Similarity 47.7%; Pred. No. 8.3e-24;  
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;  
 QY 2 QDWLTQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPKAICKGIASKN 57  
 Db 1 QDWLTQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPKAICKGIASKN 56  
 QY 58 VLTSEFYLSDC---NVTSPKCKYKLLKKSITTFCTGCENQAPVHFGVGHG 105  
 Db 60 VLTSTFQALNTCTRTSITPRPCYSSTETNYICVACENQAPVHFGVGHG 110

## RESULT 3

ID LECG RANJA STANDARD; PRT; 111 AA.  
 AC P18839;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-).  
 OS Rana japonica (Japanese reddish frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoma;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8402;  
 RN [1]

SEQUENCE, AND DISULFIDE BONDS.

RC TISSUE=Egg;

RA MEDLINE=9103519; PubMed=2229005;

RX Kamiya Y., Oyama F., Sakakibara F., Nitta K., Kawachi H.,

RA Takayama Y., Tani K.;

RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.";

RL J. Biochem. 108:139-143(1990).

CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN PREPARENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.

CC -1- SUBUNIT: Monomer.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: JX0120; JX0120.

DR HSSP: P11916; 1BC4.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase\_Pc.1.

DR PROSITE: PS00127; RNASE\_PANCREATIC.1.

KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;

KM Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1

FT ACT\_SITE 10 10 BY SIMILARITY.

FT ACT\_SITE 35 35 BY SIMILARITY.

FT ACT\_SITE 104 104 BY SIMILARITY.

FT DISULFID 19 72

FT DISULFID 34 82

FT DISULFID 52 97

FT DISULFID 94 111

SO SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

Query Match 47.2%; Score 273.5; DB 1; Length 111;

Best Local Similarity 43.2%; Pred. No. 4.3e-23;

Matches 48; Conservative 20; Mismatches 36; Indels 7; Gaps 2;

OY 2 QDMLTFOKHLNTRDVCNMLSTNLF---HCKDKNTFYISRPPEVPAICKGIASKN 57

DB 1 QWMAFKFEGHINTSINNTIMDKSIYVGGCKERNFTFISSBDNVAKICSGVSPDK 60

OY 58 VITSEFYLSDC---NVTSRPCKYKXKSTIFCYTCENQAVHPVGVCHC 105

DB 61 VLSTTFQMLNCTIRSATAPPCPYNSTRFTNVCVCKENRLEPHVHAGIGRC 111

RESULT 4

RNPL\_RANCA STANDARD; PRT; 111 AA.

AC P14626;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribonuclease, liver (EC 3.1.27.5).

OS Rana catesbeiana (Bull. frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

OX NCB1\_TaxID=8400;

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=90130374; PubMed=2613682;

RX Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,

RA Okazaki T., Ohgi K., Irie M.;

RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.";

RL J. Biochem. 106:729-735(1989).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: JX0085; JX0085.

DR HSSP: P11916; 1BC4.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase\_Pc.1.

DR PROSITE: PS00127; RNASE\_PANCREATIC.1.

KW Hydrolyase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1

FT ACT\_SITE 10 10 BY SIMILARITY.

FT ACT\_SITE 35 35 BY SIMILARITY.

FT ACT\_SITE 104 104 BY SIMILARITY.

FT DISULFID 19 72

FT DISULFID 34 82

FT DISULFID 52 97

FT DISULFID 94 111

SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 44.4%; Score 257.5; DB 1; Length 111;

Best Local Similarity 41.4%; Pred. No. 2.4e-21;

Matches 46; Conservative 20; Mismatches 38; Indels 7; Gaps 2;

OY 2 QDMLTFOKHLNTRDVCNMLSTNLF---HCKDKNTFYISRPPEVPAICKGIASKN 57

DB 1 QWMAFKFEGHINTSINNTIMDKSIYVGGCKERNFTFISSBDNVAKICSGVSPDK 60

OY 58 VITSEFYLSDC---NVTSRPCKYKXKSTIFCYTCENQAVHPVGVCHC 105

DB 61 VLSTTFQMLNCTIRSATAPPCPYNSTRFTNVCVCKENRLEPHVHAGIGRC 111

RESULT 5

RNPL\_ICUG STANDARD; PRT; 119 AA.

AC P80287;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).

OS Iguana iguana (Common iguana).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodactylidae; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.

OX NCB1\_TaxID=8517;

RP SEQUENCE.

RC TISSUE=Pancreas;

RX MEDLINE=94139745; PubMed=8307028;

RX Zhao W., Beintema J.J., Hofsteenge J.;

RT "The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.";

RT Eur. J. Biochem. 219:641-646(1994).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Pancreas.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: S4111; S4111.

DR HSSP: P0656; 1LSQ.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase\_Pc.1.

DR PROSITE: PS00127; RNASE\_PANCREATIC.1.

KW Hydrolyase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1

FT ACT\_SITE 10 10 BY SIMILARITY.

FT ACT\_SITE 35 35 BY SIMILARITY.

FT ACT\_SITE 104 104 BY SIMILARITY.

FT DISULFID 19 72

FT DISULFID 34 82

FT DISULFID 52 97

FT DISULFID 94 111

SO SEQUENCE 113 AA; 113 MW; BY SIMILARITY.

SQ	SEQUENCE	119 AA;	13324 MM;	6072FB587B15BD5A CRC64;
Query Match	24.7%;	Score 143;	DB 1;	Length 119;
Best Local Similarity	29.8%;	Pred. No. 7.9e-09;		
Matches	34;	Conservative 20;	Mismatches 44;	Indels 16; Gaps 5.
Oy	2	ODMLTFPCKHL-----TNTRDVDCNNLT---STNLPHCKDKNPTIYSRPEDVKAC--K 50		
Dd	1	QDWSFQKHLDYDETSASNPNAVCDLMMQRRLNLPYCKCRKNRFVHASPSEIQQVCSSG 60		
Oy	51	GIAASKNVLTSE--FYLSDDC-----NVTSRPCPKYKLKASTITFCVCAENQAPHF 99		
Dd	61	GTHIEDNLVDNSNESFDLTDCKANGVGTAASSCKKYNTPETKTRIRICENNQPPHF 114		

## RESULT 6

ID	ANGR_MOUSE	STANDARD;	PRT;	145 AA.
AC	064438:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Angiogenin-related protein precursor.			
GN	ANGRP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129; TISSUE=Liver;			
RA	MEDLINE=96079109; PubMed=8530072;			
RT	Brown M.E., Noble V., Subramanian V., Shapiro R.;			
RT	"the mouse angiogenin gene family: structures of an angiogenin-related			
RT	protein gene and two pseudogenes.";			
RL	Genomics 29:200-206(1995).			
CC	-1- SMILABILITY: Belongs to the pancreatic ribonuclease family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			

DR	EMBL; U22519; AAA91367.1; -.
DR	HSSP; P03950; 1A4Y.
DR	MCD; MG1; I04984; AngRp.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; rnaaseA; 1.
DR	PRINTS; PRD0794; RIBONUCLEASE.
DR	ProDom; PD000535; RNaseA; 1.
DR	SMART; SMO0092; RNase_PC; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
KM	Signal; Hydrolase; Nuclease; Endonuclease;
KW	pyroglutamate carboxylic acid.
FT	SIGNAL
FT	CHAIN
FT	MOD_RES
FT	ACT_SITE
FT	ACT_SITE
FT	ACT_SITE
FT	DISULFID
FT	DISULFID
FT	DISULFID
SO	SEQUENCE

Query Match	22.0%	Score 127.5;	DB 1;	Length 145;
Best Local Similarity	38.2%	Pred. No. 4.8e-07;		
Matches 29;	Conservative 11;	Mismatches 29;	Indels 7;	Gaps 3;

**Oy**      31 CDDKNFITSREBPVALIC--KGIILASNOV-LITSEFLDCCNTSR----PCRYKLAKS 83  
         | | | | |  
**Dd**      63 CKDVNFHIDTKNIATCAICKGKSGPYGNLRLISKSRFVTTCTHKGRSPRPCCRYRASKG 122  
         | | | | |  
**Oy**      84 TIFCVTCENOAIVHF 99  
         | | | | |  
**Dd**      123 FRIYIIIGCENGMPVHF 138

**RESULT 7**

ANG1_CERAE	STANDARD;	PRT;	146 AA.
AC	08NW66;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Angiopeasin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).		
GN	ANG OR RNASE5.		
OS	Cercopithecus aethiops (Green monkey) (Griwet).		
OC	Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Cercopithecus.		
OX	NCBI_TaxID=9534;		

RN SEQUENCE FROM N.A.  
 RP MEDLINE=21918422; PubMed=11919285;  
 RX Zhang J., Rosenberg H.F.:  
 RA "diversifying selection of the tumor-growth promoter angiogenin in  
 RT primate evolution."; Mol. Biol. Evol. 19:438-445(2002).  
 RL  
 CC -1- FUNCTION: MAY FUNCTION AS A TENA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, THEREBY  
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAs (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
CC  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC at the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC

DR	EMBL; AF441664; AAL61646.1; -.	
DR	Interpro; IPR001427; RNaseA.	
DR	Pfam; PF000074; rnaasea; 1.	
DR	ProDom; PD000535; RNasea; 1.	
DR	SMART; SM00092; RNase_Pc; 1.	
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.	
kw	Hydrolase; Nuclease; Endonuclease; Angiogenesis;	
kw	Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.	
FT	CHAIN	1 24
FT	SIGNAL	1 24
FT	MOD_RES	25 146 25
FT		
FT	ACT_SITE	37 37
FT	ACT_SITE	64 64
FT	ACT_SITE	138 138
FT	DISULFID	50 105
FT	DISULFID	63 116
FT	DISULFID	81 131
SQ	SEQUENCE	146 AA; 16444 MW; 27860112E85B8DF9 CRC64;

Query Match:	22.0%	Score 127.5:	DB 1:	Length 146:
Best Local Similarity:	30.7%	Pred. No. 4.9e-07:		
Matches	31:	Conservative	17:	Mismatches 30:
				Indels 23:
				Gaps 4
6	TFQKGLINTRDVDCNNILSTNLFCHCKDKNTFIYSRDEPKAIC--KGIASKNV-LTT	61		

```

Db      53 TWRRLRLTSP-----CKDINTFIHGRHRIKALICDENGPNVGENIRISK 97
Oy      62 SEFYLSDCNVTN-----RCKYKLKSTITFCVTCENQAPVH 98
Db      98 SPFOVTTCNLRGSGPRPCOYRATRGSRNMIWVGCENGLPVH 138

RESULT 8
RNP_GALMU
ID      RNP_GALMU      STANDARD:      PRT;      124 AA.
AC      P00680;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN      RNASE1 OR RNS1.
OS      Galea musteloides (Cui's).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Galea.
OX      NCBI_TaxId=10146;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=87036770; PubMed=6571219;
RA      Belntema J.J., Neuteboom B.;
RT      "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT      of the amino acid sequences with those of two close relatives:
RT      capybara and cuis ribonuclease.";
RL      J. Mol. Evol. 19:145-152(1983).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphonucleosides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Pancreas.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR      HSSP; P00656; ISRN.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnasea; 1.
DR      PRINTS; PR00794; RIBONUCLEASE.
DR      ProDom; PD000535; RNasea; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolase; Nuclease; Endonuclease.
FT      DISULFID 26 84 BY SIMILARITY.
FT      DISULFID 40 95 BY SIMILARITY.
FT      DISULFID 58 110 BY SIMILARITY.
FT      DISULFID 65 72 BY SIMILARITY.
FT      ACT_SITE 12 12 BY SIMILARITY.
FT      ACT_SITE 41 41 BY SIMILARITY.
FT      ACT_SITE 119 119 BY SIMILARITY.
FT      VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ      SEQUENCE 124 AA; 13870 MW; 609C7E51A7BBA25 CRC64;

Query Match 21.6%; Score 125; DB 1; Length 124;
Best Local Similarity 29.8%; Pred. No. 7.6e-07;
Matches 36; Conservative 19; Mismatches 34; Indels 32; Gaps 7;

Oy      5 LTFQGH-----TNRDVDCNNIL---STNLFHCXDXNFISRPPEVAICKGIIA 54
Db      6 MKFOQHNDSDHPTNTN--YCNEWVRKSRMTGRCRKFVNFTVHEPLAVAVC-----S 59
Oy      55 SKNV-----LTSEFYLSDCNVTNRP-----CKYKLKSTITFCVTCEN--QAPVH 98
Db      60 QKNVCKNGKQNTVCYQSHSSMRITDCRVTSSKYPKCSYRMTQAGSIIVACGTPSVPH 119
Oy      99 F 99
Db      120 F 120

RESULT 9
ANGI_BOVIN

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ID      ANGI_BOVIN      STANDARD:      PRT;      148 AA.
AC      P10152; O9GKP9;
DT      01-MAR-1989 (Rel. 10, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Angiogenin-1 precursor (EC 3.1.27.-).
GN      ANGI OR ANG.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxId=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Chang S.-I.;
RT      "Cloning, sequencing, and expression of bovine angiogenin.";
RL      Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE OF 24-148.
RC      TISSUE=Milk;
RX      MEDLINE=89065101; PubMed=3197838;
RA      Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT      "The complete amino acid sequence of bovine milk angiogenin.";
RL      FEBS Lett. 241:41-45(1988).
RN      [3]
RP      SEQUENCE OF 24-148.
RC      TISSUE=Plasma;
RX      MEDLINE=89375344; PubMed=2775757;
RA      Bond M.D., Strydom D.J.;
RT      "Amino acid sequence of bovine angiogenin.";
RL      Biochemistry 28:6110-6113(1989).
RN      [4]
RP      CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC      TISSUE=Plasma;
RX      MEDLINE=89118214; PubMed=3064806;
RA      Bond M.D., Vallee B.L.;
RT      "Isolation of bovine angiogenin using a placental ribonuclease
RT      inhibitor binding assay.";
RL      Biochemistry 27:6282-6287(1988).
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX      MEDLINE=95224057; PubMed=7708754;
RA      Acharya K.R., Shapiro R., Rordan J.F., Vallee B.L.;
RT      "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN      [6]
RP      STRUCTURE BY NMR.
RX      MEDLINE=96280645; PubMed=8688423;
RA      Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT      "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT      resonance spectroscopy.";
RL      Biochemistry 35:8870-8880(1996).
RN      [7]
RP      FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
RP      TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
RP      ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RP      PROMOTING THE ENDOGENOUS AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RP      FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
RP      MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
RP      HYDROLYZING CELLULAR TENAS. BINDS TIGHTLY TO PLACENTAL
RP      RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
RN      [8]
RP      SUBCELLULAR LOCATION: Secreted.
RN      [9]
RP      TISSUE SPECIFICITY: SERUM, AND MILK.
RN      [10]
RP      SIMILARITY: Belongs to the pancreatic ribonuclease family.
RN      [11]
RP      The SWISS-PROT entry is copyright. It is produced through a collaboration
RP      between the Swiss Institute of Bioinformatics and the EMBL outstation
RP      the European Bioinformatics Institute. There are no restrictions on its
RP      use by non-profit institutions as long as its content is in no way
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RP      entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
RP      or send an email to license@ebi.ac.uk).

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Db 6 MKFORHMDSGNSPGNNPNVNCNMMRRKMTQGRCKPVNTFVHESLEDYKAVC-----SQK 61  
 OY 57 NWL-----TSEFLSDCNVTSRP-----CKTKLKSKSTTTCVTGQNO--AAVHP 99  
 Db 62 NWLCXNGRTNCEYNSTHMTDRCQRTGSSKYPNCAYKTSQKXHIIVACEGNPYVEVHF 120

## RESULT 12

ANGI\_MOUSE  
 ID ANGI\_MOUSE STANDARD; PRT; 146 AA.  
 AC Q8WNG3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).  
 GN ANG OR RNASE5.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21918422; PubMed=11919285;  
 RA Zhang J., Rosenberg H.F.;  
 RT "Diversifying selection of the tumor-growth promoter angiogenin in primate evolution";  
 RL Mol. Biol. Evol. 19:438-445(2002).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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 CC -----  
 CC EMBL: AF41667; AAL61649.1; -;  
 CC InterPro: IPR001427; RNaseA.  
 CC Pfam: PF00074; RNaseA; 1.  
 CC ProDom: PD000535; RNaseA; 1.  
 CC SMART: SM00092; RNase\_Pc; 1.  
 CC PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 CC DR Hydroxylase; Nuclease; Endonuclease; Angiogenesis;  
 CC KM Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.  
 CC FT SIGNAL 1 24  
 CC FT CHAIN 25 146  
 CC FT MOD\_RES 25 25  
 CC FT ACT\_SITE 37 37  
 CC FT ACT\_SITE 64 64  
 CC FT ACT\_SITE 138 138  
 CC FT DISULFID 50 105  
 CC FT DISULFID 63 116  
 CC FT DISULFID 81 131  
 CC SEQUENCE 146 AA; 16301 MW; E39A89215B2A2A4 CRC64;

Query Match 20.4%; Score 118.5; DB 1; Length 146;  
 Best Local Similarity 28.7%; Pred. No. 4.7e-06;  
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

OY 6 TFOCKHLNTRDVCNNLSTLPHCKDKNTFIYSRPEVKAIC--KGIILSKAV-LTT 61  
 Db 53 TWRKRLTSP-----CKDINTFVHGNNRHHTAIICDENGSPYGNLRIST 97

OY 62 SEFLYSDCNVTS-----RCKYKTKSKSTTTCVTGQNOAPHN 98  
 Db 98 SPFOVTTCKLRGSGPRPCQYRATRGSRNIIWGCENGLPVH 138

## RESULT 13

ANGI\_MOUSE  
 ID ANGI\_MOUSE STANDARD; PRT; 145 AA.  
 AC P21570;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).  
 GN ANG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91025023; PubMed=2222458;  
 RA Bond M.D., Vallee B.L.;  
 RT "Isolation and sequencing of mouse angiogenin DNA";  
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=serum;  
 RX MEDLINE=91192291; PubMed=8448182;  
 RA Bond M.D., Strydom D.J., Vallee B.L.;  
 RT "Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and regions";  
 RL Biochim. Biophys. Acta 1162:177-186(1993).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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 CC -----  
 CC EMBL: U22516; AAA91366.1; -;  
 CC PIR: A35932; A35932.  
 CC HSSP: P03950; 1AAY.  
 CC MGD: MGI:88022; Ang.  
 CC InterPro: IPR001427; RNaseA.  
 CC Pfam: PF00074; RNaseA; 1.  
 CC PRINTS: PR00794; RIBONUCLEASE.  
 CC ProDom: PD000535; RNaseA; 1.  
 CC SMART: SM00092; RNase\_Pc; 1.  
 CC PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 CC KM Hydroxylase; Nuclease; Endonuclease; Angiogenesis;  
 CC KW Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.  
 CC FT SIGNAL 1 24  
 CC FT CHAIN 25 145  
 CC FT MOD\_RES 25 25  
 CC FT ACT\_SITE 37 37  
 CC FT ACT\_SITE 64 64  
 CC FT ACT\_SITE 137 137  
 CC FT DISULFID 50 104  
 CC DISULFID 63 115

Query Match 20.4%; Score 118.5; DB 1; Length 146;  
 Best Local Similarity 28.7%; Pred. No. 4.7e-06;  
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

OY 6 TFOCKHLNTRDVCNNLSTLPHCKDKNTFIYSRPEVKAIC--KGIILSKAV-LTT 61  
 Db 53 TWRKRLTSP-----CKDINTFVHGNNRHHTAIICDENGSPYGNLRIST 97

[illegible]

SQ	SEQUENCE	146 AA;	16432 MM;	AAC3CED1482370FE CRK64;
Query March	19.9%:	Score 115.5;	DB 1:	length 146;
Beeb Local Similarity	28.7%:	Pred. No. 9.9e-06;		
Matches	29;	Conservative 16;	Mismatches 33;	Indels 23; Gaps 4
QY	6	TFOKKHLTNRDVEDCNILSTNLPHCKDKXFIYSRPEPVAKC----	KGIASKNV-LTT	61
	::: :: :	:: :: :: :	::	::: :
Dd	53	TMRRLHLLSP-----	CDNTFTFHGNRRHHIAALCGDENGNGNPFYGCLRLISK	97
QY	62	SEFLSDCNV----TSRPCKRYLKKSSITTFCTVENQA	PVH	98
	:: :: :	:: :: :	:: :: ::	::: :
Dd	98	SFQVTTCKLHGSGPRPCRCYRAIRGSGNNIYVGCE	NGLP	138

ID	NAME	PROGU	STANDARD	PRT	128 AA
AC	P04059				
DT	01-NOV-1986	(Rel. 03, Created)			
DT	01-NOV-1986	(Rel. 03, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNaase 1) (RNaase A)				
DE	RNaase 1 OR RNaase 1				
OS	Proechimys guayanae (Castroagu)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys				
OX	NCBI_taxonomy:10163;				
RN	(1)				
RP	SEQUENCE				
RC	TISSUE=Pancreas;				
RX	MEDLINE=83000399; PubMed=7115727;				
RA	Beintema J.J., Knol G., Martens B.;				
RT	"The primary structures of pancreatic ribonucleases from African				
RT	porcupine and castreaga, two hystriocomorph rodent species."				
RL	Biochim. Biophys. Acta 705:102-110(1982).				
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-				
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P				
CC	with 2',3'-cyclic phosphate intermediates.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- TISSUE SPECIFICITY: Pancreas.				
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.				
DR	PIR: A00821; NRKS.				
DR	HSSP: P00656; 1SRN.				
DR	InterPro: IPR001427; RNaaseA.				
DR	Pfam: PF00074; rnaaseA. 1.				
DR	PRINTS: PR00794; RIBONUCLEASE.				
DR	ProDom: PD000535; RNaaseA; 1.				
DR	SMART: SMO0092; RNaase_Fc; 1.				
DR	PROSITE: PS00127; RNaase_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.				
FT	DISULFID 26 84 BY SIMILARITY.				
FT	DISULFID 40 95 BY SIMILARITY.				
FT	DISULFID 58 110 BY SIMILARITY.				
FT	DISULFID 65 72 BY SIMILARITY.				
FT	ACT_SITE 12 12 BY SIMILARITY.				
FT	ACT_SITE 41 41 BY SIMILARITY.				
FT	ACT_SITE 119 119 BY SIMILARITY.				
FT	CARBOHYD 34 34 N-LINKED (GLCNAC. . .).				
SQ	SEQUENCE 128 AA; 14244 MW; 2D858093A9D3C936 CRC64;				
Query Match	19.7%; Score 114; DB 1; Length 128;				
Best Local Similarity	29.1%; Fred. NO. 1.2e-05;				
Matches	34; Conservative 19; Mismatches 36; Indels 28; Gaps 7				
QY	7 FQKHGL-----TNRDVCNNIL-STNLF--HCKDKNFIYSRPPVAICKGIASIKV 58				
DB	8 FQKHIDSSGSPSTNPVNCNMAMKSRMTGRCKRPVNFVHEPLADVQAVC-----FQKGV 63				
QY	59 -----LTSEFPIIDCVNISR-----PCKYKLKSKSTTFCTYCTGEO--APHP 99				
DB	64 PCKNGQSNCEYSTSNMHTDRLTSNSKFPDCLVRYTSGSEKSIIVACGNGPVVPHF 120				

Search completed: January 22, 2004, 12:02:09  
Job time : 7.29213 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 : Search time 25.9551 Seconds

(without alignments)  
1043.940 Million cell updates/sec

Title: US-09-622-613c-8

Perfect score: 580

Sequence: 1 MODULFQKHLNTRDVC.....TFCVTCENQAPVHFGVGHIC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	97.6	127	13	Q918V8
2	544	93.8	127	13	Q8UUV5
3	392.5	67.7	129	13	Q9DFI6
4	374	64.5	128	13	Q9DFY8
5	299	51.6	128	13	Q9DFY7
6	297	51.2	128	13	Q9DFY5
7	286	49.3	133	13	Q98SM0
8	280	48.3	133	13	Q98SM1
9	274	47.2	133	13	Q98SM2
10	273	47.1	132	13	Q98SM3
11	270	46.6	133	13	Q98SM4
12	268	46.2	132	13	Q98SM5
13	263.5	45.4	132	13	Q9DF78
14	152.5	26.3	169	13	Q9W738
15	125	21.6	157	11	Q9JK19
16	124	21.4	157	11	Q9JKJ3

17	123	21.2	152	11	Q9JK15	Q9JK15 mus saxicol
18	123	20.8	153	11	Q9JK14	Q9JK14 meriones un
19	120.5	20.8	153	11	Q9JK17	Q9JK17 mus saxicol
20	120	20.7	157	11	Q9JKJ1	Q9JKJ1 meriones un
21	119	20.5	157	11	Q9JKJ2	Q9JKJ2 meriones un
22	117	20.2	154	11	Q9JKI8	Q9JKI8 mus saxicol
23	114.5	19.7	155	11	Q9JKI9	Q9JKI9 mus pahari
24	113.5	19.6	155	11	Q9JKI3	Q9JKI3 mus saxicol
25	111.5	19.2	132	6	Q9TV24	Q9TV24 galego mohe
26	111.5	19.2	155	11	Q9JKI8	Q9JKI8 mus pahari
27	110.5	19.1	155	11	Q9JKI6	Q9JKI6 mus saxicol
28	109.5	18.9	132	6	Q9TV25	Q9TV25 eulemur ful
29	109.5	18.9	155	11	Q9JKI2	Q9JKI2 mus saxicol
30	109.5	18.9	155	11	Q9JKI4	Q9JKI4 mus saxicol
31	108.5	18.7	170	6	Q9BEC1	Q9BEC1 tragulus ja
32	108	18.6	156	11	Q9JKG6	Q9JKG6 mus caroli
33	108	18.6	156	11	Q9JKI7	Q9JKI7 mus caroli
34	107.5	18.5	119	6	Q9TV32	Q9TV32 gorilla gor
35	107.5	18.5	147	6	Q9H200	Q9H200 pan troglod
36	107.5	18.5	155	11	Q9RI34	Q9RI34 ratius nov
37	107.5	18.5	155	11	Q9RI25	Q9RI25 mus musculu
38	107	18.4	156	11	Q9VHS0	Q9VHS0 mus musculu
39	107	18.4	156	11	Q9JKG7	Q9JKG7 mus caroli
40	106.5	18.4	119	6	Q9TS06	Q9TS06 cercopithec
41	106.5	18.4	119	6	Q9TV30	Q9TV30 saginus oe
42	106	18.3	124	6	Q9TSF2	Q9TSF2 bos taurus
43	106	18.3	156	11	Q9JKH4	Q9JKH4 mus caroli
44	106	18.3	156	11	Q9JKG9	Q9JKG9 mus caroli
45	106	18.3	156	11	Q9JKH5	Q9JKH5 mus caroli

#### ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY: PRT: 127 AA.

AC Q918V8: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DS Onconase variant rapLRL precursor.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.

OX NCBI\_TaxID=8404;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=20330357; PubMed=10871370;

RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;

RT "A gender-specific mRNA encoding a cytoxic ribonuclease contains a

RT 3' UTR of unusual length and structure."

RL Nucleic Acids Res. 28:2375-2382(2000).

DR EMBL: AF165133; AAF76935.1; -.

DR HSSP: P22069; IOWC.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase PC; 1.

DR PROSITE: PS00127; RNase\_PANCREATIC; 1.

KW Signal.

FT SIGNAL: 1 23 POTENTIAL.

FT SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

QY 2 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKXTFYSPREPVKAICGIIASKNVLT 61

DB 24 QDWLTFQKHLNTRDVCNNIMSTNLFHCKDKXTFYSPREPVKAICGIIASKNVLT 83

Query Match 97.6%, Score 566; DB 13; Length 127;

Best Local Similarity 98.1%; Pred. No. 2e-56;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	62	SEFYLSDCNVTSRPKYKLLKKSITFCVTCENQAPVHFVGVGHC	10
Db	84	SEFYLSDCNVTSRPKYKLLKKSNTFCVTCENQAPVHFVGVGHC	127
<p>RESULT 2</p> <p>Q8UVX5 PRELIMINARY; PRT; 127 AA.</p> <p>AC Q8UVX5; 20, Created)</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)</p> <p>DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)</p> <p>OS Onconase precursor.</p> <p>GN RPR.</p> <p>OS Rana pipiens (Northern leopard frog).</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele</p> <p>OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranid</p> <p>OX NCBI_TaxID=8404;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Liao Y.-D., Wang S.-C.;</p> <p>RL "Rana pipiens onconase genomic DNA.";</p> <p>RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; AF32139; AAL54383.1; -</p> <p>DR InterPro; IPR001427; RNaseA.</p> <p>DR Pfam; PF00074; rnaaseA; 1.</p> <p>DR ProDom; PD000535; RNaseA; 1.</p> <p>DR SMART; SM00092; RNase_PC; 1.</p> <p>DR PROSITE; PS00127; RNASE_PANCREATIC; 1.</p> <p>KW SIGNAL.</p> <p>FT SIGNAL</p> <p>RP SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;</p> <p>QY Query Match 93.8%; Score 544; DB 13; Length 1</p> <p>Best Local Similarity 94.28; Pred No. 6.3e-54;</p> <p>Matches 98; Conservative 3; Mismatches 3; Indels</p>			
Qy	2	QDWLTFOKKHILTNTRDVCNIIKKSITFCVTCENQAPVHFVGVGHC	105
Db	24	QDWLTFOKKHILTNTRDVCNIIKKSNTFCVTCENQAPVHFVGVGHC	127
<p>RESULT 3</p> <p>Q8DFY6 PRELIMINARY; PRT; 129 AA.</p> <p>AC Q8DFY6; 16, Created)</p> <p>DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)</p> <p>DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)</p> <p>DE RC-RNase4 ribonuclease precursor.</p> <p>OS Rana catesbeiana (Bull frog).</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele</p> <p>OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranid</p> <p>OX NCBI_TaxID=8400;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA TISSUE=Liver;</p> <p>RC TISSUE=Liver;</p> <p>EX MEDLINE=20512555; PubMed=11058105;</p> <p>RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wan</p> <p>RT "Purification and cloning of cytotoxic ribonucleases from</p> <p>RL catesbeiana (bullfrog).";</p> <p>RT Nucleic Acids Res. 28:4097-4104(2000).</p> <p>RN [2]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RC TISSUE=Liver;</p> <p>RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wan</p> <p>RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; AF242555; AAC31441.2; -</p> <p>DR HSP; P22069; 10NC.</p>			

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ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR ProDom; PD000535; RNaseA.1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT CHAIN 1 23
FT SIGNAL RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 51.6%; Score 299; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 3.7e-26;
Matches 55; Conservative 13; Mismatches 36; Indels 0; Gaps 0;

QY 2 QDWLFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 61
DB 24 QDWTFQKKHLTDTKKVKCDVEMKALFDCKKTNTFIYALPGRVKAICKNRDNDVLSR 83

QY 62 SEFYLSDCNVTSPCKYKLLKSTITFCVTCENQAPVHFVGVC 105
DB 84 DAFLLPQCDRIKLPCHYKLSSTNTICITCVNQLPIHFAGVGC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR ProDom; PD000535; RNaseA.1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

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KW SIGNAL.
FT CHAIN 1 23
FT SIGNAL RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFBFB67D266C7C2 CRC64;

Query Match 51.2%; Score 297; DB 13; Length 128;
Best Local Similarity 51.9%; Pred. No. 6.2e-26;
Matches 54; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

QY 2 QDWLFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 61
DB 24 QDWTFQKKHLTDTKKVKCDVEMKALFDCKKTNTFIYALPGRVKAICKNRDNDVLSR 83

QY 62 SEFYLSDCNVTSPCKYKLLKSTITFCVTCENQAPVHFVGVC 105
DB 84 DVFYLPQCNRRKKLPCHYRLDGSNTICITCMKELPIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR ProDom; PD000535; RNaseA.1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT CHAIN 1 22
FT SIGNAL POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 49.3%; Score 286; DB 13; Length 133;
Best Local Similarity 47.7%; Pred. No. 1.1e-24;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

QY 2 QDWLFQKKHLTNRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QNWATFQKKHITNTSSINCNTIMDNIIYVGGQCKGVNTFISSATTVKAICTGVI-NMN 81

QY 58 VLTTSSEFVLSDC--NVTSRCKYKLLKSTITFCVTCENQAPVHFVGVC 105
DB 82 VLSTTRFQNTCTRTSTTPPCPISSRTENNIVICVKCENQVPHFAGVGC 132

RESULT 8
Q9PWR7 PRELIMINARY; PRT; 133 AA.
AC Q9PWR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

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OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165025; PubMed=9497370;
RT Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL; AF039104; AAD10702.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 48.3%; Score 280; DB 13; Length 133;
Best Local Similarity 47.7%; Pred. No. 5.4e-24;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

OY 2 QWLTFFQKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QNWATFQKHITNTSSINCNMNLSYIVGGCKKVTFIASSATTVKAICTGVI-NMN 81

OY 58 VLTTFSEFYLSDC---NVTSRPCKYKLLKSKTITFCVTCENQAPVHFVGVGHC 105
DB 82 VLSTTRFQKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57

RESULT 9
OY Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21539506; PubMed=11683320;
RT Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351207; AAK30253.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 47.1%; Score 273; DB 13; Length 132;
Best Local Similarity 45.9%; Pred. No. 3.3e-23;
Matches 51; Conservative 15; Mismatches 37; Indels 8; Gaps 3;

OY 2 QWLTFFQKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QWAKFQKHIPSTSSINCNTIMDNNIYIVGGCKKVTFIASSATTVKAICNG-VTNSN 81

OY 58 VLTTFSEFYLSDC---NVTSRPCKYKLLKSKTITFCVTCENQAPVHFVGVGHC 105
DB 82 VLSTTRFQKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 132

RESULT 11
OY Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21539506; PubMed=11683320;
RT Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351210; AAK30256.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 47.2%; Score 274; DB 13; Length 133;
Best Local Similarity 45.9%; Pred. No. 2.6e-23;
Matches 51; Conservative 18; Mismatches 34; Indels 8; Gaps 3;

OY 2 QWLTFFQKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QNWATFQKHITNTSSINCNMNLSYIVGGCKKVTFIASSATTVKICSG-VTDKK 81
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RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAK30257.1; -.
DR HSSP; P11916; 18C4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A9AFASB943 CRC64;

Query Match 46.6%; Score 270; DB 13; Length 133;
Best Local Similarity 45.0%; Pred. No. 7.4e-23;
Matches 50; Conservative 19; Mismatches 34; Indels 8; Gaps 3;

Qy 2 QDWLTFQKHILNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db 23 QNWATFQKHITPSSIDCNIMNLSYIVGQCKKVTFTIASSATTVKIGICSG-VTDKK 81

Qy 58 VLTSEFYLSDCN---VTSRPPCKYKLKSTITFCVTCENQAPVHFVGVGHC 105
Db 82 VLSSTKFOLDICTRIFITPRPCPSSTRTETNYICVKCENQVPHFAGIGQC 132

RESULT 12
Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1,
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN SIGNAL.
RN MEDLINE=21539506; PubMed=11683320;
RP Kirschner M.W., Zhang J., Liao Y.-D., Dyer K.D.;
RP "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 18C4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 46.2%; Score 268; DB 13; Length 132;
Best Local Similarity 46.8%; Pred. No. 1.2e-22;
Matches 52; Conservative 15; Mismatches 36; Indels 8; Gaps 3;

Qy 2 QDWLTFQKHILNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db 23 QDWLTFQKHITPSSIDCNIMNLSYIVGQCKKVTFTIYSATTVKICTGVLSN-N 81

Qy 58 VLTSEFYLSDCN---VTSRPPCKYKLKSTITFCVTCENQAPVHFVGVGHC 105
Db 82 VLSSTRQLXXXTFTITSRPPCVSSSTKETNKICVKCENQVPHFAGIGKC 132

RESULT 13
Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78,
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
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DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RN Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSSP; P11916; 18C4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452PBE53 CRC64;

Query Match 45.4%; Score 263.5; DB 13; Length 132;
Best Local Similarity 42.3%; Pred. No. 4e-22;
Matches 47; Conservative 20; Mismatches 37; Indels 7; Gaps 2;

Qy 2 QDWLTFQKHILNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db 22 QNWAKFKEKHITPSSIDCNIMNLSYIVGQCKKERTFIISSEDNVKALCSGVSPDRK 81

Qy 58 VLTSEFYLSDCN---NVTSPCKYKLKSTITFCVTCENQAPVHFVGVGHC 105
Db 82 ELSTTSFKLNTCIRDSITPRPCPYHPSDNNKICVKCEKQLPVHFVGVGKC 132

RESULT 14
Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738,
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kirschner M.W., Minshall J., Kirschner M.W.;
RA "The identification of two novel ligands of the FGF receptor by a
RT yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630(1995).
RN [2]
RN SEQUENCE FROM N.A.
RA Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159166; AAD41901.1; -.
DR HSSP; P00656; ILSQ.
DR InterPro; IPR001427; RNaseA.
```

DR Pfan; PF00074; rnaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match 26.3%; Score 152.5; DB 13; Length 169;  
Best Local Similarity 36.1%; Pred. No. 1.9e-09;  
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;

QY 7 FOKKHLTNT-RDVDCN-----NILSTNLFHCKDKNTFY-SRPEPVKAICKGIIASKNV 58  
DB 33 FWEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90  
QY 59 LTTSEFYLSDCNV---TSRP--CKYKLLKXSTITFCVTCENQAPVHVG 101  
DB 91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTGTGVIINTCENNYPVHFAG 138

RESULT 15

Q9JKI9 PRELIMINARY; PRT; 157 AA.

AC Q9JKI9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE 01-NAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Eosinophil-associated ribonuclease 44.  
GN EAR44.  
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Meriones.  
OX NCBI\_TaxID=10047;  
RN [1]

SEQUENCE FROM N.A.  
RX MEDLINE=20243759; PubMed=10758160;  
RA Zhang J., Dyer K.D., Rosenberg H.F.;  
RT "Evolution of the rodent eosinophil-associated ribonuclease gene  
family by rapid gene sorting and positive selection."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).  
DR EMBL; AF238394; AAF67694.1; -.  
DR HSSP; P10153; 1HI2.  
DR InterPro; IPR001427; RNaseA.  
DR Pfan; PF00074; rnaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;

Query Match 21.6%; Score 125; DB 11; Length 157;  
Best Local Similarity 30.3%; Pred. No. 2.4e-06;  
Matches 33; Conservative 21; Mismatches 35; Indels 20; Gaps 7;

QY 4 WLTFQKKHLTNTRDVDCN-NILSTNLF--HCKDKNTFYSRPEPV-----KAICKGII 53  
DB 36 WFTIQ--HISNTTTTCNAAMLGVANNYGRCKDLNLTFLTRFANYVNECYNNTTCKN-- 91  
QY 54 ASKNVL-TTSEFYLSDCNVTS-----RPCKYKLLKXSTITFCVTCENQAP 96  
DB 92 GRNCHDSRSKVSITDCNLTSFANSYRQCYQRYTRARFYRIACNNKTP 140

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.65169 Seconds  
(without alignments)  
784.758 Million cell updates/sec

Title: US-09-622-613c-17

Perfect score: 607

Sequence: 1 MNWATFOQKHINTPIICN.....ICVKCENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591.5	97.4	111	1 RNP0_RANCA	P11916 rana cateeb
2	455	75.0	111	1 LECS_RANCA	P18039 rana japoni
3	374	61.6	111	1 RNP1_RANCA	P14626 rana cateeb
4	277.5	45.7	104	1 RNP3_RANPI	P22069 rana pipien
5	154.5	25.5	145	1 ANG3_MOUSE	P97802 mus musculus
6	149.5	24.6	145	1 ANGR_MOUSE	Q64438 mus musculus
7	135.5	22.3	124	1 RNP_BALAC	P00673 balaenopter
8	135.5	22.3	145	1 ANGI_MOUSE	P21570 mus musculus
9	133.5	22.0	167	1 RNP0_BOVIN	P39873 bos taurus
10	132.5	21.8	124	1 RNP_PIG	P00671 sus scrofa
11	131.5	21.7	119	1 RNP_IGUIG	P80287 iguana igua
12	128.5	21.2	151	1 RNP1_CAPCA	P79351 capreolus c
13	127.5	21.0	123	1 ANG2_BOVIN	P80929 bos taurus
14	127.5	21.0	141	1 RNP1_GIRCA	Q29542 giraffa cam
15	127.5	21.0	151	1 RNP1_AXIPR	P87350 axis porcin
16	125	20.6	146	1 ANGI_SAISS	Q8wn60 saimiri sci
17	124	20.4	146	1 ANGI_MIOTA	Q8wn65 miopithecus
18	123.5	20.3	143	1 RNP1_SHEEP	Q29543 ovis aries
19	122.5	20.2	124	1 RNP1_ANTAM	P00668 antilocapra
20	122.5	20.2	146	1 ANGI_CERAB	Q8wn66 cercopithec
21	122	20.1	122	1 RNP1_MACRO	P00676 macropus r
22	120.5	19.9	128	1 RNP1_MYOCO	P00676 myocastor c
23	120.5	19.9	149	1 RNP1_MOUSE	P00683 mus musculus
24	120.5	19.8	146	1 ANGI_AOTTR	Q8wn61 aotus trivi
25	120	19.8	147	1 ANGI_PONPY	Q8wn67 pongo pygma
26	119.5	19.7	123	1 ANGI_PIG	P31346 sus scrofa
27	118.5	19.5	128	1 RNP1_CAVPO	P00679 cavia porce
28	118	19.4	146	1 ANGI_SAGOE	Q8wn62 saguinus oe
29	117.5	19.4	128	1 RNP1_HORSE	P00674 equus caball
30	116.5	19.2	124	1 RNP1_CAMDR	P00670 camelus dro
31	116.5	19.2	128	1 RNP1_PROGU	P04059 proechimys
32	115.5	19.0	146	1 ANGI1_MACMU	Q8wn63 macaca mula
33	114	18.8	148	1 ANGI1_BOVIN	P10152 bos taurus

#### ALIGNMENTS

##### RESULT 1

ID	RNP0_RANCA	STANDARD;	PRT;	111 AA.
AC	P11916;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase)			(Sialic acid-binding
DE	lectin) (SBL-C).			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
EX	MEDLINE=87299649; PubMed=3304421;			
RA	Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana			
RT	catesbeiana) eggs.";			
RT	Biochemistry 26:2189-2194(1987).			
RL	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana			
RT	catesbeiana (bullfrog) oocytes.";			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,			
RA	Takayanagi Y., Hakomori S., Titani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana			
RT	catesbeiana eggs.";			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=98437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes			
RT	of Rana catesbeiana (bullfrog).";			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-I- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine			
CC	residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)			
CC	as substrates, and prefers the former. The S-lectins in frog eggs			
CC	may be involved in the fertilization and development of the frog			
CC	embryo. This lectin agglutinates various animal cells, including			
CC	normal lymphocytes, erythrocytes, and fibroblasts of animal and			
CC	human origin.			
CC	-I- SUBUNIT: Monomer.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR; A27121; A27121.			

P00666 rangifer ta  
Q8wn64 papio hamad  
P03950 homo sapien  
Q8wn68 pan troglod  
P00664 capreolus c  
P00662 giraffa cam  
Q9jjh1 mus musculu  
P31347 oryctolagus  
P24717 cricetus  
O55004 rattus norv  
Q9wt55 acomys cahi  
P07847 aepyceros m

34 113.5 18.7 124 1 RNP\_RANTA  
35 113.5 18.7 146 1 ANGI\_PAPHA  
36 113 18.6 147 1 ANGI\_HUMAN  
37 113 18.6 147 1 ANGI\_PANTR  
38 112.5 18.5 124 1 RNP\_CAPCA  
39 112.5 18.5 124 1 RNP\_GIRCA  
40 112.5 18.5 148 1 RNS4\_MOUSE  
41 112 18.5 125 1 ANGI\_RABIT  
42 111.5 18.4 130 1 RNP\_CRILO  
43 111.5 18.4 147 1 RNS4\_RAT  
44 111.5 18.4 149 1 RNP\_ACOCA  
45 110.5 18.2 124 1 RNP\_ABPME

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DR PDB; 1BC4; 28-OCT-98.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
FT HELIX 3 10
FT HELIX 19 23
FT TURN 26 27
FT STRAND 37 41
FT HELIX 45 51
FT TURN 52 52
FT STRAND 57 62
FT STRAND 68 73
FT STRAND 83 88
FT STRAND 92 97
FT TURN 98 99
FT STRAND 100 107
FT SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;
Query Match 97.4%; Score 591.5; DB 1; Length 111;
Best Local Similarity 99.1%; Pred. No. 3 8e-57;
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 60
DB 1 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 60
QY 61 LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
RESULT 2
LECS_RANJA STANDARD; PRT; 111 AA.
AC P18839;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; JX0120; JX0120.
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DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 104 104
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDBDDF3834ED679 CRC64;
Query Match 75.0%; Score 455; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 2 1e-42;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;
QY 2 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGV-INNM 59
DB 1 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGV-INNM 59
QY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 61 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENRNPVHFAGIGRCP 111
RESULT 3
RNPL_RANCA STANDARD; PRT; 111 AA.
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver.";
RL J. Biochem. 106:729-735(1989).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; JX0085; JX0085.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 104 104
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDBDDF3834ED679 CRC64;
```

[illegible]





DR GlycoSuiteDB: P39873; -.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase P; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 167 RIBONUCLEASE, BRAIN.  
 FT ACT\_SITE 38 67 BY SIMILARITY.  
 FT ACT\_SITE 67 67 BY SIMILARITY.  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT DISULFID 52 110 BY SIMILARITY.  
 FT DISULFID 66 121 BY SIMILARITY.  
 FT DISULFID 84 136 BY SIMILARITY.  
 FT DISULFID 91 98 BY SIMILARITY.  
 FT CARBOHYD 88 88 /FTID=CAR\_000005.  
 FT CARBOHYD 155 155 O-LINKED.  
 FT CARBOHYD 159 159 O-LINKED.  
 FT CONFLICT 155 155 T -> S (IN REF. 2).  
 SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;  
 Query Match 22.0%; Score 133.5; DB 1; Length 167;  
 Best Local Similarity 31.4%; Pred. No. 1.7e-07;  
 Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;  
 QY 5 ATFOQKH-----INTPIICNTIMDNIIYVGGQCKRVNTFIISATTVAICTGVINM 58  
 DB 32 AKPRHMDSSGSSSNPNYCNQMRR-RMTHGRCKPVPNTFVHESLDVKAACS---QK 87  
 QY 59 NVL-----STTRFOLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHFA 105  
 DB 88 NITCKGNHCNVCQSKSTMSITDCRETGSSKYPNCAYKTSQOKYITVACEGPPVPVPHFD 147  
 QY 106 G 106  
 DB 148 G 148  
 RESULT 10  
 RNP\_PIG STANDARD; PRT; 124 AA.  
 AC P00671;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
 GN RNASE1 OR RNS1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70104197; PubMed=5460946;  
 RA Jackson R.L., Hirs C.H.W.;  
 RT "The primary structure of porcine pancreatic ribonuclease. II. The amino acid sequence of the reduced S-aminoethylated protein.";  
 RL J. Biol. Chem. 245:637-653 (1970).  
 RN [2]  
 RP REVISION TO 2.  
 RA Wierenga R.K., Huizinga J.D., Gaastera W., Welling G.W., Beintema J.J.;  
 RT "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence.";  
 RL FEBS Lett. 31:181-185 (1973).  
 RN [3]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=70104198; PubMed=4904878;  
 RA Phelan J.J., Hirs C.H.W.;  
 RT "The primary structure of porcine pancreatic ribonuclease. 3. The disulfide bonds.";

RL J. Biol. Chem. 245:654-661 (1970).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Pancreas.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PIR: A92071; NRPG.  
 DR HSSP: P00656; 1SRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase P; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84  
 FT DISULFID 40 95  
 FT DISULFID 58 110  
 FT DISULFID 65 72  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. .).  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. .).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. .).  
 SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;  
 Query Match 21.8%; Score 132.5; DB 1; Length 124;  
 Best Local Similarity 31.6%; Pred. No. 1.6e-07;  
 Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;  
 QY 7 FOQKH-----INTPIICNTIMDNIIYVGGQCKRVNTFIISATTVAICTGV-INNM 59  
 DB 8 FORQMDPSSSSSNPNYCNLMMSRR-NMTQGRCKPVPNTFVHESLADVQAVCSQINVK 66  
 QY 60 VLSTTRFOLNT-----CTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHVF 104  
 DB 67 NGQTCYQSNSTMTHTDCRQTGSSKYPNCAYKASQOKHIVACEGPPVPVPHF 120  
 RESULT 11  
 RNP\_IGUIG STANDARD; PRT; 119 AA.  
 AC P80287;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
 OS Iguana iguana (Common iguana).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
 OX NCBI\_TaxID=8517;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94139745; PubMed=8307028;  
 RA Zhao W., Beintema J.J., Hofsteenge J.;  
 RT "The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.";  
 RL Eur. J. Biochem. 219:641-646 (1994).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Pancreas.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PIR: S41111; S41111.  
 DR HSSP: P00656; 1LSQ.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.



DR SMART; SM00092; RNase P; 1.  
 KW PROSITE; PS00127; RNase P; 1.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 25 80 BY SIMILARITY.  
 FT DISULFID 39 91 BY SIMILARITY.  
 FT DISULFID 57 106 BY SIMILARITY.  
 FT ACT\_SITE 10 10 BY SIMILARITY.  
 FT ACT\_SITE 40 40 BY SIMILARITY.  
 FT ACT\_SITE 113 113 BY SIMILARITY.  
 SQ SEQUENCE 119 AA; 13324 MW; 6072F85B7B15BD5A CRC64;

Query Match 21.7%; Score 131.5; DB 1; Length 119;  
 Best Local Similarity 30.4%; Pred. No. 28-07;  
 Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

OY 2 QNATFOQKH-----INTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAIC-- 52  
 DB 1 QMSSFFQKHIDYPTASNPAYCDLMMQRR-NLNPCKTKRNTFVHASPSEIQOVCS 59  
 OY 53 --TGVINNVLSSTTRFQNTCTRTSIT-PRPCYSSRTETNYICVKCNQYVPHF 104  
 DB 60 GGTHYEDNLYDSNESFDLTCKNVGSGTAPSSCKYNGTCTKEIRACENNQVPHF 114

RESULT 12  
 ID RNBR CAPCA STANDARD; PRT; 151 AA.  
 AC P79351;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 25-DEC-1998 (Rel. 37, Last sequence update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Capreolus capreolus (Roe deer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
 OC Cervidae; Odocoileinae; Capreolus.  
 OX NCBI\_TaxID=9858;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98278842; PubMed=9611269;  
 RA Bruckelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,  
 RA Beintema J.J.;  
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";  
 RL Gene 212:259-268(1998).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/ebis-sib.ch/announcements>  
 CC or send an email to [license@ebi-sib.ch](mailto:license@ebi-sib.ch)).  
 CC EMBL; Y11673; CAA72371.1; -.  
 DR HSSP; P00656; 1SRN.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase P; 1.  
 DR PROSITE; PS00127; RNase P; 1.  
 DR Hydrolyase; Nuclease; Endonuclease; 1.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 65 72 BY SIMILARITY.  
 FT CARBOHYD 62 62 N-LINKED (GLCNAC... (BY SIMILARITY).  
 FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).  
 FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).

SQ SEQUENCE 151 AA; 16971 MW; 392D0B6302F006A6 CRC64;

Query Match 21.2%; Score 128.5; DB 1; Length 151;  
 Best Local Similarity 29.4%; Pred. No. 5.4e-07;  
 Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;

OY 5 ATFOQKH-----INTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAIC-- 58  
 DB 6 AKFRQHMDSGSSSGNPNYCNQMMKR-RWTHGCKPNTFVHESLDNVKAVCS--OK 61  
 OY 59 NVL-----STTRFQNTCTRTSITPRP-CYSSRTETNYICVKCENQ--YVPHF 104  
 DB 62 NITCKNGQPCYQSNSTWNTIDCRQTGSSKYPNCAYKTSQOKYITVACEGDPYVPHF 120

RESULT 13  
 ID ANG2 BOVIN STANDARD; PRT; 123 AA.  
 AC P80929;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE Angiogenin-2 (EC 3.1.27.-).  
 DE Angiogenin-2 (EC 3.1.27.-).  
 GN ANG2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Milk, and Serum;  
 RX MEDLINE=97409980; PubMed=9266695;  
 RA Straydom D.J., Bond M.D., Vallee B.L.;  
 RT "An angiogenic protein from bovine serum and milk -- purification and  
 RT primary structure of angiogenin-2.";  
 RL Eur. J. Biochem. 247:535-544(1997).  
 CC -!- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR RNAs.  
 CC -!- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR HSSP; P10152; 1AGI.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase P; 1.  
 DR PROSITE; PS00127; RNase P; 1.  
 DR Hydrolyase; Nuclease; Endonuclease; 1.  
 KW Protein synthesis inhibitor; Glycoprotein;  
 KW Pyrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 39 39 BY SIMILARITY.  
 FT ACT\_SITE 113 113 BY SIMILARITY.  
 FT DISULFID 25 80  
 FT DISULFID 38 91  
 FT DISULFID 56 106  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC...).  
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 123;  
 Best Local Similarity 30.6%; Pred. No. 5.5e-07;  
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

OY 7 FOQKHINTPI-----ICNTIMDNNIYVGGCKRVNTFISSATTVKAIC--TGVINM 58  
 DB 8 FLRKHYPSTGHDDRYCINTWERR--NMTRPCKDTNTFIHNSDDIRAVCDNRNGEYR 65  
 OY 59 NVLSTTR--FQNTCTRTSITPR-PCYSSRTETNYICVKCENQYVPH 103

[illegible]

Db 122 G 122

Search completed: January 22, 2004, 12:02:09  
Job time : 6.65169 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 26.3989 Seconds  
(without alignments)  
869.271 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATFQKHINTPIICN.....ICVKCENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
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  - 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	100.0	111	11	US-09-961-400-17
2	602	99.2	110	11	US-09-948-391A-15
3	602	99.2	110	11	US-09-961-400-15
4	602	99.2	111	11	US-09-948-391A-26
5	602	99.2	111	11	US-09-961-400-26
6	601	99.0	111	11	US-09-948-391A-17
7	601	99.0	111	11	US-09-948-391A-21
8	601	99.0	111	11	US-09-961-400-21
9	601	99.0	117	11	US-09-948-391A-22
10	601	99.0	117	11	US-09-961-400-22
11	597	98.4	110	11	US-09-948-391A-24
12	597	98.4	110	11	US-09-961-400-24
13	596	98.2	110	11	US-09-961-400-19
14	590	97.2	110	11	US-09-948-391A-19
15	286.5	47.2	105	11	US-09-948-391A-6

16	286.5	47.2	105	11	US-09-961-400-6	Sequence 6, Appli
17	283.5	46.7	111	11	US-09-961-400-9	Sequence 9, Appli
18	282.5	46.5	105	15	US-10-153-882-2	Sequence 2, Appli
19	281.5	46.4	104	11	US-09-961-400-2	Sequence 2, Appli
20	281.5	46.4	105	11	US-09-948-391A-13	Sequence 13, Appli
21	281.5	46.4	105	11	US-09-961-400-13	Sequence 13, Appli
22	281.5	46.4	127	11	US-09-948-391A-28	Sequence 28, Appli
23	281.5	46.4	127	11	US-09-961-400-28	Sequence 28, Appli
24	280.5	46.2	104	11	US-09-948-391A-2	Sequence 2, Appli
25	280.5	46.2	105	11	US-09-961-400-8	Sequence 8, Appli
26	276.5	45.6	104	11	US-09-948-391A-11	Sequence 11, Appli
27	276.5	45.6	104	11	US-09-961-400-11	Sequence 11, Appli
28	275.5	45.4	104	11	US-09-948-391A-4	Sequence 4, Appli
29	275.5	45.4	104	11	US-09-961-400-4	Sequence 4, Appli
30	272.5	44.9	104	10	US-09-986-119-1	Sequence 1, Appli
31	272.5	44.9	104	11	US-09-918-887-1	Sequence 1, Appli
32	271.5	44.7	105	11	US-09-948-391A-8	Sequence 8, Appli
33	271.5	44.7	111	11	US-09-948-391A-9	Sequence 9, Appli
34	206	33.9	83	10	US-09-986-119-3	Sequence 3, Appli
35	206	33.9	83	11	US-09-918-887-3	Sequence 3, Appli
36	163	26.9	169	13	US-10-016-447-2	Sequence 2, Appli
37	131.5	21.7	119	12	US-10-074-978A-139	Sequence 139, App
38	121	19.9	99	12	US-10-074-978A-141	Sequence 141, App
39	117	19.3	147	10	US-09-731-872-254	Sequence 254, App
40	117	19.3	147	12	US-09-876-997-254	Sequence 254, App
41	114.5	18.9	124	10	US-09-981-286A-8	Sequence 8, Appli
42	114	18.8	124	13	US-10-016-447-5	Sequence 5, Appli
43	113	18.6	131	13	US-10-016-447-6	Sequence 6, Appli
44	113	18.6	147	9	US-09-286-240-6	Sequence 6, Appli
45	113	18.6	147	9	US-09-863-777-2	Sequence 2, Appli

## ALIGNMENTS

### RESULT 1

US-09-961-400-17  
; Sequence 17, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-17

Query Match	100.0%	Score	607	DB	11	Length	111
Query Local Similarity	100.0%	Pred. No.	1.8e-61				
Matches	111	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MQNWATFQKHINTPIICNTIMDNNIYVGGCKRVNTFIISATVKAICTGVINNV	60				
Db	1	MQNWATFQKHINTPIICNTIMDNNIYVGGCKRVNTFIISATVKAICTGVINNV	60				
Qy	61	LSTTRFQNTCTRTSTTPRCPVSSRTETNYICVKCENQYVHFAGIGRCP	111				
Db	61	LSTTRFQNTCTRTSTTPRCPVSSRTETNYICVKCENQYVHFAGIGRCP	111				

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RESULT 2
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match          99.2%; Score 602; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.6e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 61
Db 1 QNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60

Oy 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 3
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15
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Query Match          99.2%; Score 602; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.6e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 QNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 61
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Oy 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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RESULT 4
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26

Query Match          99.2%; Score 602; DB 11; Length 111;
Best Local Similarity 99.1%; Pred. No. 6.6e-61;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MONWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
Db 1 MSNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60

Oy 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 5
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
```



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Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MOWATFOQKHIIPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 9
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match 99.0%; Score 601; DB 11; Length 117;
Best Local Similarity 98.2%; Pred. No. 9.2e-61;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 7 MOWATFOQKHIIPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 10
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 99.0%; Score 601; DB 11; Length 117;
Best Local Similarity 98.2%; Pred. No. 9.2e-61;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 7 MOWATFOQKHIIPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 11
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
; OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

Query Match 98.4%; Score 597; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.4e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 NWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62
Db 2 NWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 12
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
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GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-24

Query Match 98.4%; Score 597; DB 11; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2.4e-60;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 62  
Db 2 NWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 61

Qy 63 TTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 111  
Db 62 TTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 13  
US-09-961-400-19  
; Sequence 19, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-19

Query Match 98.2%; Score 596; DB 11; Length 110;  
Best Local Similarity 98.2%; Pred. No. 3.2e-60;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QNWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61  
Db 1 QNWATFOOKHIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60

Qy 62 STTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 111  
Db 61 STTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 110

Db 61 STTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 14  
US-09-948-391A-19  
; Sequence 19, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: NEWTON, DIANNE L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; TITLE OF INVENTION: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and  
; OTHER INFORMATION: Met57Leu substitutions (recombinant RacOR1  
; OTHER INFORMATION: Met22Leu Met57Leu)  
US-09-948-391A-19

Query Match 97.2%; Score 590; DB 11; Length 110;  
Best Local Similarity 97.3%; Pred. No. 1.5e-59;  
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QNWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61  
Db 1 QNWATFOOKHIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60

Qy 62 STTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 111  
Db 61 STTRFQNLCTRTSITPRPCPYSSRSTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15  
US-09-948-391A-6  
; Sequence 6, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: NEWTON, DIANNE L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; TITLE OF INVENTION: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 105





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 12.4719 Seconds  
(without alignment)  
855.901 Million cell updates/sec

Title: US-09-622-613C-17  
Perfect score: 607  
Sequence: 1 MQNWATFOQKHINTPIICN.....ICVKCENQYPVHPAGIGRCP 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588.5	97.0	111	2 A27121	ribonuclease-relat
2	455	75.0	111	1 JX0120	ribonuclease-relat
3	374	61.6	111	2 JX0085	pancreatic ribonuc
4	274.5	45.2	104	2 A39035	ribonuclease-relat
5	135.5	22.3	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.3	145	1 A35932	angiogenin precurs
7	133.5	22.0	167	2 S20066	pancreatic-type ri
8	132.5	21.8	124	1 NRPQ	pancreatic ribonuc
9	131.5	21.7	119	2 S41111	pancreatic ribonuc
10	122.5	20.2	124	1 NRPH	pancreatic ribonuc
11	122	20.1	122	1 NRKGR	pancreatic ribonuc
12	120.5	19.9	128	1 NRCU	pancreatic ribonuc
13	120.5	19.9	149	1 NRMS	pancreatic ribonuc
14	119.5	19.7	123	1 A43825	pancreatic ribonuc
15	118.5	19.5	128	1 NRGPB	angiogenin - pig
16	117.5	19.4	128	1 NRHO	pancreatic ribonuc
17	116.5	19.2	124	1 NRCM	pancreatic ribonuc
18	116.5	19.2	124	1 NRCMM	pancreatic ribonuc
19	116.5	19.2	124	1 NRCMB	pancreatic ribonuc
20	116.5	19.2	128	1 NRKS	pancreatic ribonuc
21	114.5	18.9	124	2 S08549	ribonuclease - dom
22	114	18.8	125	1 A32474	angiogenin [valida
23	113.5	18.7	124	1 NRDEN	pancreatic ribonuc
24	113	18.6	147	1 NRHUAG	angiogenin precurs
25	112.5	18.5	124	1 NRFG	pancreatic ribonuc
26	112.5	18.5	124	1 NRDEO	pancreatic ribonuc
27	112	18.5	125	1 B43825	angiogenin - rabbi
28	111.5	18.4	130	2 S22808	pancreatic ribonuc
29	110.5	18.2	124	1 NRBOB	pancreatic ribonuc

30	110.5	18.2	124	1 NRWB	pancreatic ribonuc
31	110.5	18.2	124	1 NREKN	pancreatic ribonuc
32	110.5	18.2	124	2 S07141	pancreatic ribonuc
33	110.5	18.2	150	1 NRBO	pancreatic ribonuc
34	110.5	18.2	158	2 I61900	eosinophil-derived
35	109.5	18.0	124	1 NRSH	pancreatic ribonuc
36	108.5	17.9	119	2 JX0115	pancreatic ribonuc
37	108.5	17.9	124	1 NRCB	pancreatic ribonuc
38	108.5	17.9	152	1 NRRT	pancreatic ribonuc
39	106.5	17.5	124	1 NRHP	pancreatic ribonuc
40	106.5	17.5	125	4 A47498	seminal ribonuclea
41	106.5	17.5	150	1 NRBO	ribonuclea
42	104.5	17.2	124	1 NRGN	pancreatic ribonuc
43	104.5	17.2	124	1 NRDEF	pancreatic ribonuc
44	104	17.1	125	2 S04503	pancreatic ribonuc
45	103.5	17.1	124	2 S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121  
ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi,

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <111>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 97.0%; Score 588.5; DB 2; Length 111;  
Best Local Similarity 98.2%; Pred. No. 1.4e-51;  
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy	2	QNWATFOQKHINTPII	CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVNNV	60
Db	1	ENWATFOQKHINTPIINC	NTIMDNIIYVGQCKRVNTFIISATTVKAICTGVNNV	60
Qy	61	LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP	111	
Db	61	LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP	111	

RESULT 2

JX0120  
ribonuclease-related sialic acid-binding lectin - Japanese frog

C:Species: Rana japonica (Japanese frog)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: JX0120

R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi,

J. Biochem. 108, 139-143, 1990

A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A:Reference number: JX0120; MUID:91035319; PMID:2229005

A:Accession: JX0120

A:Molecule type: protein

A:Residues: 1-111 <KAM>

A:Experimental source: egg

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin; pyroglytamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.0%; Score 455; DB 1; Length 111;  
Best Local Similarity 78.4%; Pred. No. 2.6e-38;  
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

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OY 2 QNWATFOQKHINTP-IICNTIMDNIIYVGGCKRVNTFISSATTVAICTGV-INNN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QNWAQFQKHINTSNINCNTIMDKSIYVGGCKRVNTFISSATTVAICSGASTRN 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 60 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHPFAGIGRC 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENRLDPVHPFAGIGRC 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, K.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, T.;
J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglyutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10.35.104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 61.6%; Score 374; DB 2; Length 111;
Best Local Similarity 65.8%; Pred. No. 2.9e-30;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

OY 2 QNWATFOQKHINTPII-CNTIMDNIIYVGGCKRVNTFISSATTVAICTGVI-NNN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QNWAQFQKHIRSTSIDCNTIMDKAIYVGGCKRVNTFISSADNVKAICSGVSPDRK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 60 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHPFAGIGRC 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ELSTTSFKLNTCIRDSTPRPCPYHSPDNNKICVKCEKQLPVHPVGIGKC 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A:Reference number: A39035; MUID:91093131; PMID:1985896
A:Accession: A39035
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match 45.2%; Score 274.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.1e-20;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

OY 2 QNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVAICTGVI-NNN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EDWLTFQKHINTTRDVEDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 60 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHPFAGIGRC 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 57 VLTTFSEFYLSDC---NVTSRPKYKLLKSTNFKFCVTCBNQAPVHPVGVC 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
```

```
N:Alternate names: RNase 1; RNase A
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:26-84,40-55,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.3%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.7e-06;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

OY 7 FQKHII-----NTPICNTIMDNIIYVGGCKRVNTFISSATTVAICTGVINMNV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 FQKHMDSGNSPGNNPNYCNQMMRR-RDTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 L-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 LCKNGRTNYESNTMHTDCRQTGSSKYPNCAYTSOKERHIIIVACEGNPVVPHF 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:222458
A:Accession: A35932
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BN>
A:Cross-references: GB:U22516; NID:G726325; PIDN:AAA91366.1; PID:G726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglyutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37.64.137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.3%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 2e-06;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

OY 34 CKRVNTFISSATTVAIC---TGVINMNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 88
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 CKDVNTFIHGNKSNIKAIKANGANGSPYRENLRMSKSPFOVTTCKHTGGSPRPPCQYRASG 122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 89 TNYICVKCENQYVPHF 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 FRHVVIACENGLPVHF 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
```

S20066  
 pancreatic-type ribonuclease (EC 3.1.1.27.5) Brb precursor, brain - bovine  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 22-Jun-1999  
 C/Accession: S20066; JX0056  
 R:Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri  
 Nucleic Acids Res. 19, 6469-6474, 1991  
 A>Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex  
 A/Reference number: S20066; MUID:92093604; PMID:1754384  
 A/Accession: S20066  
 A/Molecule type: DNA  
 A/Residues: 1-167 <SAS>  
 A/Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151  
 R:Matanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri  
 J. Biochem. 104, 939-945, 1988  
 A>Title: Primary structure of a ribonuclease from bovine brain.  
 A/Reference number: JX0056; MUID:89214015; PMID:3243767  
 A/Accession: JX0056  
 A/Molecule type: protein  
 A/Residues: 27-154, 'S', 156-166 <WAT>  
 A/Experimental source: brain  
 C/Superfamily: pancreatic ribonuclease  
 C/Keywords: Glycoprotein; hydrolase  
 F:38,67,145/Active site: His, Lys, His #status predicted  
 F:52-110,66-121,84-136,91-98/Disulfide bonds: #status experimental  
 F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match	22.0%	Score 133.5;	DB 2;	Length 167;
Best Local Similarity	31.4%;	Pred. No. 3.6e-06;		
Matches	38;	Conservative	17;	Mismatches 43; Indels 23; Gaps 7;

Qy 5 ATFOQKH-----INTPICTNTIMDNVIVGSOCKRVNTEIISSATTVKAICTGVINM 58  
 Db 32 AKFRQRMDSGSSSSPNVCNQMVKR-RMTVGRCKPVNIFVHESLDDVKAICS---QK 87  
 Qy 59 NVL-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105  
 Db 88 NITCKNGHPNCYOSKSTMSITDCRETGSSKYPNCAYKTSQKQVITVACEGPNFVPVHPD 147  
 Qy 106 G 106  
 Db 148 G 148

RESULT 8  
 NRPG  
 Pancreatic ribonuclease (EC 3.1.1.27.5) - pig  
 N/Alternate names: RNase 1; RNase A  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
 C/Accession: A92071; A91391; A00816  
 R:Jackson, R.L.; Hirs, C.H.W.  
 J. Biol. Chem. 245, 637-653, 1970  
 A>Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se  
 A/Reference number: A92071; MUID:70104197; PMID:5460946  
 A/Accession: A92071  
 A/Molecule type: protein  
 A/Residues: 1,'O',3-124 <JAC>  
 R:Wierenga, R.K.; Huizinga, J.D.; Gassetta, W.; Welling, G.W.; Beintema, J.J.  
 FEBS Lett. 31, 181-185, 1973  
 A>Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation  
 A/Reference number: A91391  
 A/Accession: A91391  
 A/Molecule type: protein  
 A/Residues: 1-124 <WIE>  
 R:Phelan, J.J.; Hirs, C.H.W.  
 J. Biol. Chem. 245, 654-661, 1970  
 A>Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo  
 A/Reference number: A92072; MUID:70104198; PMID:4904878  
 A/Contents: annotation; disulfide bonds  
 C/Superfamily: pancreatic ribonuclease

```

Db      6 AKFERQHIDSNPSSVSSSYCHNOMKSR-NLTQGRCKPNTFVHESLADVOAVCS---QK 61
Qy      59 NYL-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
Db      62 NVACKNGOTNCYQSYSTWSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGPNYPVPHV 120

RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo
N:Alternate names: RNase 1; RNase A
C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C:Accession: A00833
R:Gaaststra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A:Reference number: A00833; MUID:78190621; PMID:658039
A:Accession: A00833
A:Molecule type: protein
A:Residues: 1-122 <GAA>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:11,40,117/Active site: His, Lys, His #status predicted
F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match      20.1%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.6e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 10; Gaps 6;

Qy      7 FQKH-----INTPIICNTIMDNNIYVIGOCKRVNTFISSATTVKAIC----- 52
Db      7 FORQMDTEHSTASSNYCNLMKAR-DWTSGRCLPLTFIHEPKSVDAVCHQENVTCK 65

Qy      53 TGVINNVLSITRFLQNLCTRTSITPRP-CPYSSRTETNYICVKENQY-PVHF 104
Db      66 NGRNTC-YKSNRSLSTNCQTGASKYPNCQYETSNLKQIIVACEGQYVPVHF 118

RESULT 12
NRUC
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A0612; MUID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: protein
A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match      19.9%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.4e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

Qy      7 FQKH-----INTPIICNTIMDNNIYVIGOCKRVNTFISSATTVKAICTGVINNV 60
Db      8 FERQHMDSRGSPSTPNVNEWMKSR-NNTQGRCKPNTFVHEPLADVOAVC---FQRNV 63

Qy      61 L-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
Db      64 LCKNGOTNCYQSNMHIIDCRVTSNSDYPNCYSYRTSQEKSIVACEGPNYPVPHF 120

```

```

RESULT 13
NRMS
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse
N:Alternate names: RNase 1; RNase A
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: A34090; S22598; A00830
R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A:Reference number: A34090; MUID:90136034; PMID:2299980
A:Accession: A34090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <SCH>
A:Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A:Reference number: S22598; MUID:92107684; PMID:1840677
A:Accession: S22598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <SAM>
A:Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R:Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 96, 399-408, 1979
A:Title: The amino acid sequence of mouse pancreatic ribonuclease.
A:Reference number: A00830; MUID:80024269; PMID:556267
A:Accession: A00830
A:Molecule type: protein
A:Residues: 26-149 <LEN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F:37,66,144/Active site: His, Lys, His #status predicted
F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      19.9%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

Qy      7 FQKH-----INTPIICNTIMDNNIYVIGOCKRVNTFISSATTVKAICTGVINNV 60
Db      33 FORQMDPDGSSINSPTYCNQMKRR-DWTGSCRPVNTFVHEPLADVOAVCS---QENV 88

Qy      61 L-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
Db      89 TCKNRKSNCKYKSSSALHITDCHLKSGSKYPNCYDKYKTQYQKHIIVACEGPNYPVPHF 145

RESULT 14
A43825
angiogenin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29834; A43825
R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29834
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-123 <BON>
A:Note: this sequence was submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease

Query Match      19.7%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.5e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:30 : Search time 13.3034 Seconds  
(without alignments)  
353.031 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATFQKHINTPIICN.....ICVKENQVPHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	97.0	111	2	US-08-891-848-12
2	588.5	97.0	111	3	US-08-875-811-8
3	284.5	46.9	104	1	US-08-467-955-2
4	279.5	46.0	105	3	US-08-875-811-39
5	279.5	46.0	355	3	US-08-875-811-41
6	279.5	46.0	358	3	US-08-875-811-51
7	277.5	45.7	104	3	US-09-394-268-1
8	277.5	45.7	104	4	US-09-687-748-1
9	277.5	45.7	112	3	US-08-875-811-32
10	277.5	45.7	129	3	US-08-875-811-63
11	277.5	45.7	251	3	US-08-875-811-59
12	277.5	45.7	254	3	US-08-875-811-61
13	277.5	45.7	355	3	US-08-875-811-49
14	277.5	45.7	355	3	US-08-875-811-57
15	277.5	45.7	355	3	US-08-875-811-64
16	277.5	45.7	366	3	US-08-875-811-55
17	277.5	45.7	379	3	US-08-875-811-43
18	274.5	45.2	104	1	US-08-283-971-1
19	274.5	45.2	104	1	US-07-921-619-1
20	274.5	45.2	104	1	US-08-467-955-1
21	274.5	45.2	104	2	US-08-891-848-13
22	272.5	44.9	104	3	US-08-875-811-1
23	272.5	44.9	104	3	US-09-394-268-2
24	272.5	44.9	104	4	US-09-071-672-1
25	272.5	44.9	104	4	US-09-687-748-2
26	272.5	44.9	105	3	US-08-875-811-26
27	272.5	44.9	106	3	US-08-875-811-28

28 272.5 44.9 107 3 US-08-875-811-30  
29 271.5 44.7 105 3 US-08-875-811-24  
30 268.5 44.2 358 3 US-08-875-811-45  
31 268.5 44.2 365 3 US-08-875-811-53  
32 250.5 41.3 107 3 US-08-875-811-20  
33 239.5 39.5 111 3 US-08-875-811-22  
34 236 38.9 114 3 US-09-223-118-3  
35 232.5 38.3 360 3 US-08-875-811-47  
36 227 37.4 114 3 US-09-223-118-2  
37 226 37.2 114 3 US-09-223-118-1  
38 225 37.1 114 3 US-09-223-118-4  
39 206 33.9 83 3 US-08-875-811-2  
40 206 33.9 83 4 US-09-071-672-3  
41 163 26.9 169 1 US-08-441-629-2  
42 163 26.9 169 3 US-08-776-207-2  
43 163 26.9 169 4 US-09-507-773-2  
44 163 26.9 169 5 PCT-US95-09172-2  
45 124.5 20.5 125 6 5171845-2

#### ALIGNMENTS

#### RESULT 1

US-08-891-848-12  
; Sequence 12, Application US/08891848  
; Patent No. 5955073  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Youle, Richard J.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Nicholls, Peter J.  
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,848  
; FILING DATE: No. 5955073 yet assigned  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,462  
; FILING DATE: 22-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/014,082  
; FILING DATE: 04-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/779,195  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/510,696  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-110310US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid

Sequence 30, Appl  
Sequence 24, Appl  
Sequence 45, Appl  
Sequence 53, Appl  
Sequence 20, Appl  
Sequence 22, Appl  
Sequence 3, Appl  
Sequence 47, Appl  
Sequence 2, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Patent No. 5171845

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
; US-08-891-848-12
Query Match 97.0%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 5e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
;
Qy 2 QNWATFOOKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 ENWATFOOKHIIINTPIINCNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Farris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111

; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
; US-08-875-811-8
Query Match 97.0%; Score 588.5; DB 3; Length 111;
Best Local Similarity 98.2%; Pred. No. 5e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
;
Qy 2 QNWATFOOKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 ENWATFOOKHIIINTPIINCNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardeit Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467.955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
```



DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-2

Query Match 46.0%; Score 284.5; DB 1; Length 104;  
Best Local Similarity 49.1%; Pred. No. 9.1e-26;  
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

Oy 2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NM 59  
Db 1 EDWLTFOQKHINTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56  
Oy 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110  
Db 57 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFCVTCENQAPVHFVGVGSC 104

## RESULT 4

US-08-875-811-39  
; Sequence 39, Application US/08875811  
; Patent No. 6045793

GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Boque, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,800  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-875-811-39

Query Match 46.0%; Score 279.5; DB 3; Length 105;  
Best Local Similarity 49.1%; Pred. No. 3.5e-25;  
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Oy 1 MQNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NM 58  
Db 1 MEDWLTFOQKHINTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56  
Oy 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110

Db 57 NVLTTSFYLSDC---NVTSRPCKYKLKSTNKFCVTCENQAPVHFVGVGSC 105

## RESULT 5

US-08-875-811-41  
; Sequence 41, Application US/08875811  
; Patent No. 6045793

GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Boque, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,811  
; FILING DATE: 19-FEB-1998  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/02588  
; FILING DATE: 19-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,800  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Faris, Susan K.  
; REGISTRATION NUMBER: 41,739  
; REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-875-811-41

Query Match 46.0%; Score 279.5; DB 3; Length 355;  
Best Local Similarity 49.1%; Pred. No. 1.6e-24;  
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Oy 1 MQNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NM 58  
Db 251 MEDWLTFOQKHINTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 306  
Oy 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110  
Db 307 NVLTTSFYLSDC---NVTSRPCKYKLKSTNKFCVTCENQAPVHFVGVGSC 355

## RESULT 6

US-08-875-811-51  
; Sequence 51, Application US/08875811  
; Patent No. 6045793

GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Boque, Lluís

```

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Farris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-51

Query Match 46.0%; Score 279.5; DB 3; Length 358;
Best Local Similarity 49.1%; Pred. No. 1.6e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 MNWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOKKHINTNRDVCNIMSTNLP----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 NVLTTFEYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 7
US-09-394-268-1
; Sequence 1, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 45.7%; Score 277.5; DB 3; Length 104;
Best Local Similarity 49.5%; Pred. No. 5.9e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKKHINTNRDVCNIMSTNLP----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTFEYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 8
US-09-687-748-1
; Sequence 1, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 5.9e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKKHINTNRDVCNIMSTNLP----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTFEYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 9
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Liuis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-32

Query Match 45.7%; Score 277.5; DB 3; Length 112;
Best Local Similarity 49.1%; Pred. No. 6.5e-25;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MQNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 8 MSDWLTFOQKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63

Qy 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 64 NVLTSEFVLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 112

RESULT 10
US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-32

Query Match 45.7%; Score 277.5; DB 3; Length 112;
Best Local Similarity 49.1%; Pred. No. 6.5e-25;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MQNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 8 MSDWLTFOQKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63

Qy 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 64 NVLTSEFVLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 112

RESULT 11
US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-59

Query Match 45.7%; Score 277.5; DB 3; Length 251;
Best Local Similarity 49.1%; Pred. No. 1.7e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
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Oy 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 147 MSDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIITASK 202

Oy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 203 NVLTTSFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 251

RESULT 12
US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011.800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-61

Query Match 45.7%; Score 277.5; DB 3; Length 254;
Best Local Similarity 49.1%; Pred. No. 1.8e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Oy 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MSDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIITASK 56

Oy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 NVLTTSFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 105

RESULT 13
US-08-875-811-49
; Sequence 49, Application US/08875811
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```
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011.800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-49

Query Match 45.7%; Score 277.5; DB 3; Length 355;
Best Local Similarity 49.1%; Pred. No. 2.7e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Oy 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 251 MSDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIITASK 306

Oy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 307 NVLTTSFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 355

RESULT 14
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 27.4382 Seconds  
(without alignment)  
1043.940 Million cell updates/sec

Title: US-09-622-613c-17

Perfect score: 607

Sequence: 1 MQNWATPQKHINTPIICN.....ICVKCNQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mic:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591.5	97.4	133	13 Q9PWR7	Q9pwr7 rana catesb
2	560.5	92.3	133	13 Q98SM0	Q98sm0 rana catesb
3	487.5	80.3	132	13 Q98SM2	Q98sm2 rana catesb
4	478.5	78.8	133	13 Q98SL9	Q98sl9 rana catesb
5	471.5	77.7	133	13 Q98SL8	Q98sl8 rana catesb
6	448.5	73.9	132	13 Q98SM1	Q98sm1 rana catesb
7	376	61.9	132	13 Q9DF78	Q9df78 rana catesb
8	281.5	46.4	127	13 Q918V8	Q918v8 rana pipien
9	277.5	45.7	127	13 Q8UVX5	Q8uvx5 rana pipien
10	246	40.5	129	13 Q9DFY6	Q9dfy6 rana catesb
11	229.5	37.6	128	13 Q9DFY8	Q9dfy8 rana catesb
12	226.5	37.3	128	13 Q9DFY7	Q9dfy7 rana catesb
13	217.5	35.8	128	13 Q9DFY5	Q9dfy5 rana catesb
14	163	26.9	169	13 Q9W738	Q9w738 xenopus lae
15	131	21.6	170	6 Q9BEC1	Q9bec1 tragus ja
16	126	20.8	150	11 Q8VD94	Q8vd94 beryimys bo

17	125.5	20.7	163	6 Q9BDC2	Q9bdc2 antilocapra
18	124.5	20.5	116	6 Q9TVC0	Q9tvc0 sus scrofa
19	124	20.4	150	11 Q8VD88	Q8vd88 rattus norv
20	122.5	20.2	144	6 Q9BH14	Q9bh14 antilocapra
21	120.5	19.9	149	11 Q8K2T2	Q8k2t2 mus musculu
22	120.5	19.9	149	11 Q8CGG3	Q8cgg3 mus musculu
23	120	19.8	150	11 Q8VD92	Q8vd92 rattus exul
24	116.5	19.2	152	11 Q8VD89	Q8vd89 rattus norv
25	115.5	19.0	119	6 Q9TV13	Q9tv13 bos taurus
26	114.5	18.9	124	6 Q95NE6	Q95ne6 bubalus bub
27	112.5	18.5	148	11 Q8C7E4	Q8c7e4 mus musculu
28	112.5	18.5	149	11 Q8VD95	Q8vd95 beryimys bo
29	112	18.5	134	6 Q9BDB9	Q9bdb9 tragus ja
30	111.5	18.4	152	11 Q8VD84	Q8vd84 rattus tiom
31	111.5	18.4	156	6 Q8SQ05	Q8sq05 lagotrix l
32	111	18.3	148	11 Q8C663	Q8c663 mus musculu
33	110.5	18.2	119	6 Q9TV28	Q9tv28 eulemur ful
34	110.5	18.2	119	6 Q9TV10	Q9tv10 saginus oe
35	110.5	18.2	124	6 Q9TSF2	Q9tsf2 bos taurus
36	109.5	18.0	142	6 Q9BEC3	Q9bec3 tragus ja
37	109.5	18.0	156	6 Q8SQ06	Q8sq06 ateles gaof
38	109	18.0	124	6 Q9BEC2	Q9bec2 tragus ja
39	108.5	17.9	156	6 Q8SQ08	Q8sq08 saimiri sci
40	108.5	17.9	156	6 Q8SQ07	Q8sq07 saginus oe
41	107.5	17.7	152	11 Q8VD90	Q8vd90 rattus fusc
42	106.5	17.5	116	6 Q97933	Q97933 phocoenoid
43	106.5	17.5	149	11 Q8VD93	Q8vd93 rattus exul
44	105.5	17.4	116	6 Q97934	Q97934 pseudorca c
45	105.5	17.4	119	6 Q9TSQ6	Q9tsq6 cercopithec

ALIGNMENTS

RESULT 1

Q9PWR7	ID	Q9PWR7	PRELIMINARY;	PRT;	133 AA.
AC	Q9PWR7;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Ribonuclease precursor.				
GN	RCR.				
OS	Rana catesbeiana (Bull frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.				
NCBI_TaxID=8400;					
[1]					
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=98165825; PubMed=9497370;				
RA	Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;				
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.				
RT	Tissue distribution, cloning, purification, cytotoxicity, and active				
RT	residues for RNase activity."				
RL	J. Biol. Chem. 273:6395-6401(1998).				
DR	EMBL; AF039104; AAD10702.1; -.				
DR	HSP; P11916; IBC4				
DR	InterPro; IPR001427; RNaseA.				
DR	Pfam; PF00074; rnasea; 1.				
DR	ProDom; PD000535; RNaseA; 1.				
DR	SMART; SM00092; RNase_Pc; 1.				
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.				
KW	SIGNAL.				
FT	SIGNAL. 1 22 POTENTIAL.				
SQ	SEQUENCE 133 AA; 14762 MW; A7D62594F7D16FOC CRC64;				

Query Match 97.4%; Score 591.5; DB 13; Length 133;  
Best Local Similarity 99.1%; Pred.No. 4.5e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATPQKHINTPII-CNTIMNNDNIYVGGCKRVNTFIISATTVTKAICTGVINMV 60



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ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAK30257.1; -.
DR HSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FASB943 CRC64;

Query Match 77.7%; Score 471.5; DB 13; Length 133;
Best Local Similarity 76.6%; Pred. No. 2.6e-46;
Matches 85; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTYKAICTGVINNV 60
Db 23 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTYKAICTGVINNV 82

Qy 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 111
Db 83 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 133

RESULT 6
Q98SM1 PRELIMINARY; PRT; 132 AA.
AC
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760729868E CRC64;

Query Match 73.9%; Score 448.5; DB 13; Length 132;
Best Local Similarity 78.2%; Pred. No. 1.1e-43;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTYKAICTGVINNV 60
Db 23 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTYKAICTGVINNV 82

Qy 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 111
Db 83 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 133

RESULT 7
Q9DF78 PRELIMINARY; PRT; 132 AA.
AC
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452FBES3 CRC64;

Query Match 61.9%; Score 376; DB 13; Length 132;
Best Local Similarity 65.8%; Pred. No. 2.3e-35;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTYKAICTGVINNV 59
Db 22 QNWAKFKKHITSTSSIDCNDIMDKAIYIVGCKKERTNTFISSDNVKAICSGVSPDRK 81

Qy 60 VLSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 82 ELSTTSFKLNTCIRDSITPRPCPYHPYDNNKICVKCKQLPVHFVGVGKGC 132

RESULT 8
Q918V8 PRELIMINARY; PRT; 127 AA.
AC
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Onconase variant rapLRI precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760729868E CRC64;

Query Match 73.9%; Score 448.5; DB 13; Length 132;
Best Local Similarity 78.2%; Pred. No. 1.1e-43;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTYKAICTGVINNV 59
Db 22 QNWAKFKKHITSTSSIDCNDIMDKAIYIVGCKKERTNTFISSDNVKAICSGVSPDRK 81

Qy 60 VLSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 82 ELSTTSFKLNTCIRDSITPRPCPYHPYDNNKICVKCKQLPVHFVGVGKGC 132
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
  3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

  Query Match      46.4%; Score 281.5; DB 13; Length 127;
  Best Local Similarity 49.5%; Pred. No. 1.5e-24;
  Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVAICTGVI-NMN 59
DB 24 QDWLTFQKKHLNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 79

QY 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
DB 80 VLTTFSEFYLSDC---NVTSRCPKYKLKSTNFCVTENQAPVHFVGVC 127

RESULT 9
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; 953F90D351CFEF3 CRC64;

  Query Match      45.7%; Score 277.5; DB 13; Length 127;
  Best Local Similarity 49.5%; Pred. No. 4.4e-24;
  Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVAICTGVI-NMN 59
DB 24 QDWLTFQKKHLNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 79

QY 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
DB 80 VLTTFSEFYLSDC---NVTSRCPKYKLKSTNFCVTENQAPVHFVGVC 127
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RESULT 10
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
  catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

  Query Match      40.5%; Score 246; DB 13; Length 129;
  Best Local Similarity 43.4%; Pred. No. 1.9e-20;
  Matches 49; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY 2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVAICTGVI-NMN 59
DB 24 QDWATFKKHLTDWVDCNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79

QY 60 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 111
DB 80 VLSNSEFYLAEC---NVKPRPKCYKLKSSNRICRCEHELPHVHFAGVGICP 129

RESULT 11
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
  catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
```

[illegible]



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 27.191 Seconds  
(without alignments)  
1043.940 Million cell updates/sec

Title: US-09-622-613C-19  
Perfect score: 600  
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585.5	97.6	133	Q9PWR7	Q9pwr7 rana catesb
2	554.5	92.4	133	Q98SM0	Q98sm0 rana catesb
3	483.5	80.6	132	Q98SM2	Q98sm2 rana catesb
4	474.5	79.1	133	Q98SL9	Q98sl9 rana catesb
5	467.5	77.9	133	Q98SL8	Q98sl8 rana catesb
6	444.5	74.1	132	Q98SM1	Q98sm1 rana catesb
7	372	62.0	132	Q9DF78	Q9df78 rana catesb
8	277.5	46.2	127	Q9I8V8	Q9i8v8 rana pipien
9	273.5	45.6	127	Q8UVX5	Q8uvx5 rana pipien
10	243	40.5	129	Q9DFY6	Q9dfy6 rana catesb
11	225.5	37.6	128	Q9DFY8	Q9dfy8 rana catesb
12	223.5	37.2	128	Q9DFY7	Q9dfy7 rana catesb
13	214.5	35.8	128	Q9DFY5	Q9dfy5 rana catesb
14	161	26.8	169	Q9W738	Q9w738 xenopus lae
15	128	21.3	170	Q9BEC1	Q9bec1 tragulus ja
16	121.5	20.2	116	Q9TVCO	Q9tvco sus scrofa

17	121.5	20.2	163	6	Q9BDC2	Q9bdc2 antilocapra
18	121	20.2	150	11	Q8VD94	Q8vd94 berylmys bo
19	119	19.8	150	11	Q8VD88	Q8vd88 rattus norv
20	118.5	19.8	144	6	Q9BH14	Q9bhl14 antilocapra
21	116.5	19.4	149	11	Q8K2T2	Q8k2t2 mus musculu
22	116.5	19.4	149	11	Q8C6G3	Q8c6g3 mus musculu
23	116	19.3	150	11	Q8VD92	Q8vd92 rattus exul
24	113.5	18.9	152	11	Q8VD89	Q8vd89 rattus norv
25	113.5	18.8	119	6	Q9TV33	Q9tv33 bos taurus
26	111	18.5	148	11	Q8C663	Q8c663 mus musculu
27	110.5	18.4	124	6	Q9SNE6	Q9sne6 bubalus bub
28	109.5	18.2	148	11	Q8C7E4	Q8c7e4 mus musculu
29	109.5	18.2	149	11	Q8VD95	Q8vd95 berylmys bo
30	109	18.2	124	6	Q9BEC2	Q9bec2 tragulus ja
31	109	18.2	134	6	Q9BDB9	Q9bdb9 tragulus ja
32	108.5	18.1	152	11	Q8VD84	Q8vd84 rattus tiom
33	108.5	18.1	156	6	Q8SQ05	Q8sq05 legothrix l
34	107.5	17.9	119	6	Q9TV28	Q9tv28 eulemur ful
35	107.5	17.9	119	6	Q9TV30	Q9tv30 saguinus oe
36	106.5	17.8	124	6	Q9TSF2	Q9tsf2 bos taurus
37	106.5	17.8	156	6	Q8SQ06	Q8sq06 ateles geof
38	105.5	17.6	142	6	Q9BEC3	Q9bec3 tragulus ja
39	105.5	17.6	156	6	Q8SQ08	Q8sq08 salmirl sci
40	105.5	17.6	156	6	Q8SQ07	Q8sq07 saguinus oe
41	104.5	17.4	152	11	Q8VD90	Q8vd90 rattus fusc
42	103.5	17.2	116	6	Q97933	Q97933 phocoenoide
43	103.5	17.2	149	11	Q8VD93	Q8vd93 rattus exul
44	102.5	17.1	116	6	Q97934	Q97934 pseudorca c
45	102.5	17.1	119	6	Q9TSQ6	Q9tsq6 cercopithec

ALIGNMENTS

RESULT 1

Q9PWR7 ID Q9PWR7 PRELIMINARY; PRT; 133 AA.  
AC Q9PWR7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribonuclease precursor.  
GN RCR.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP TISSUE=Liver;  
RC MEDLINE=98165825; PubMed=9497170;  
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;  
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.  
RT Tissue distribution, cloning, purification, cytotoxicity, and active  
RT residues for RNase activity.";  
RL J. Biol. Chem. 273:6395-6401(1998).  
DR EMBL; AF019104; AAD10702.1; -  
DR HSSP; P11916; IBC4.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnasea; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL. 1 22 POTENTIAL.  
FT CHAIN 23 133 RIBONUCLEASE.  
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16FOC CRC64;  
Query Match 97.6%; Score 585.5; DB 13; Length 133;  
Best Local Similarity 97.3%; Pred. No. 4.3e-59;  
Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 59



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ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rnase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
    J. Mol. Evol. 53:31-38(2001).
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AA30257.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FASB943 CRC64;

Query Match 77.9%; Score 467.5; DB 13; Length 133;
Best Local Similarity 75.7%; Pred. No. 1.3e-45;
Matches 84; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QNWATFOEQHITNTSSINCNMNSLYVGGQCKVNTFIASSATTVKICSGVTDKV 82

QY 60 LSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
Db 83 LSSTKFOLDICTRIFITPRPCPYSSRTETNYICVKCENQYVHPFAGIGQCP 133

RESULT 6
Q98SM1 PRELIMINARY; PRT; 132 AA.
ID Q98SM1;
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rnase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
    J. Mol. Evol. 53:31-38(2001).
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AA30254.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 74.1%; Score 444.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 5.4e-43;
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Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QDWPTFOQKHIPSTSSIDCNTIMDKIYIVRGQCKVNTFIYSATTVKAICTGVLSNV 82

QY 60 LSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 109
Db 83 LSTTRFOLXXXTRFITRSPCPYSSTKTNKICVKCENYVHPFAGIGKC 132

RESULT 7
Q9DF78 PRELIMINARY; PRT; 132 AA.
ID Q9DF78;
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=20512555; PubMed=11058105;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
    catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAC30414.2; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASE1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBES3 CRC64;

Query Match 62.0%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 1e-34;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 58
Db 22 QNWAKFKKHITSTSSIDCNTIMDKIYIVGGQCKRNTFIISSEDNVKACSGVSPDK 81

QY 59 VLSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 109
Db 82 ELSTTSFKLNTICRDSITPRPCPYHSPDNKNKICVKCEKQLPVHFGVIGKC 132

RESULT 8
Q918V8 PRELIMINARY; PRT; 127 AA.
ID Q918V8;
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Onconase variant rapLr1 precursor
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
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RN RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2385(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 46.2%; Score 277.5; DB 13; Length 127;
Best Local Similarity 48.6%; Pred. No. 6.1e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

OY 1 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFIISATTVAICTGVI-NLN 58
DB 24 QDWLTFQKHLTNRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 79

OY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 109
DB 80 VLTSEFYLSDC---NVTSRCKYKLLKSTNFCVTCENQAPVHFVGVC 127

RESULT 9
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEF3 CRC64;

Query Match 45.6%; Score 273.5; DB 13; Length 127;
Best Local Similarity 48.6%; Pred. No. 1.7e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

OY 1 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFIISATTVAICTGVI-NLN 58
DB 24 QDWLTFQKHLTNRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 79

OY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 109
DB 80 VLTSEFYLSDC---NVTSRCKYKLLKSTNFCVTCENQAPVHFVGVC 127

RESULT 10
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.5%; Score 243; DB 13; Length 129;
Best Local Similarity 42.5%; Pred. No. 5.4e-20;
Matches 48; Conservative 25; Mismatches 30; Indels 10; Gaps 5;

OY 1 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFIISATTVAICTGVI-NLN 58
DB 24 QDWATFKKHLTDTWDVDCNLMPTSLF---DCKDKNTFIYSLPCPVKALCRGVIFSAD 79

OY 59 VLSTTRFQNTCTRTSITPR-PCPYSSRTETNYICVKENQYVHFAGIGRC 110
DB 80 VLSNSEFYLAEC---NVKPRKPCYKLLKSSNRICRCEHELPHVHFAGVGICP 129

RESULT 11
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
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RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; --
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 5.3e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
Db 24 QNWETFOQKHLTDTRDKVCDMAEMKALF----DCKQNTFIYAPGRVQALCKNIIVSKN 79

Qy 59 VLSSTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 80 VLSTDEFYLCNRIKL---PCHYKLKSSNTICITCNKLPVHFVAVEECP 128

RESULT 12
Q9DFV7
ID Q9DFV7 PRELIMINARY; PRT; 128 AA.
AC Q9DFV7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN Nucleic Acids Res. 28:4097-4104(2000).
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 5.3e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
Db 24 QNWETFOQKHLTDTRDKVCDMAEMKALF----DCKQNTFIYAPGRVQALCKNIIVSKN 79

Qy 59 VLSSTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 80 VLSTDEFYLCNRIKL---PCHYKLKSSNTICITCNKLPVHFVAVEECP 128

RESULT 12
Q9DFV7
ID Q9DFV7 PRELIMINARY; PRT; 128 AA.
AC Q9DFV7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN Nucleic Acids Res. 28:4097-4104(2000).
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.2%; Score 223.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 9e-18;
Matches 45; Conservative 19; Mismatches 39; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
Db 24 QNWETFOQKHLTDTRDKVCDMAEMKALF----DCKQNTFIYAPGRVQALCKNIIVSKN 79

Qy 59 VLSSTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 80 VLSTDEFYLCNRIKL---PCHYKLKSSNTICITCNKLPVHFVAVEECP 128

RESULT 13
Q9DFV5
ID Q9DFV5 PRELIMINARY; PRT; 128 AA.
AC Q9DFV5
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 34.9213 Seconds  
(without alignment)  
504.524 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATFQKHIIPTIICN.....ICVKCENQYVHFAGIGRCR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 19Jun03;\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	100.0	111	20	AAV28873
2	602	99.2	110	20	AAV28872
3	602	99.2	111	20	AAV28878
4	601	99.0	111	20	AAV28876
5	597	98.4	110	20	AAV28877
6	596	98.2	110	20	AAV28874
7	588.5	97.0	111	20	AAV33321
8	286.5	47.2	105	20	AAV28867
9	284.5	46.9	104	18	AAW06544

10	283.5	46.7	105	20	AAV28869	Recombinant Met (-1
11	282.5	46.5	105	20	AAV39400	Recombinant frog O
12	281.5	46.4	104	20	AAV28865	Rana pipiens liver
13	281.5	46.4	105	20	AAV28871	Recombinant Met (-1
14	281.5	46.4	127	20	AAV28879	Rana pipiens Clone
15	279.5	46.0	105	18	AAV35123	R. pipiens recombi
16	279.5	46.0	355	18	AAV35125	R. pipiens recombi
17	279.5	46.0	358	18	AAV35130	R. pipiens recombi
18	278.5	45.9	104	20	AAV28866	Recombinant RAPUR1
19	277.5	45.7	104	18	AAW30301	Recombinant onc pr
20	277.5	45.7	104	22	AAW31666	Amino acid sequenc
21	277.5	45.7	104	23	ABG32650	Northern leopard f
22	277.5	45.7	112	18	AAW35118	R. pipiens recombi
23	277.5	45.7	251	18	AAW35134	R. pipiens recombi
24	277.5	45.7	254	18	AAW35135	R. pipiens recombi
25	277.5	45.7	355	18	AAW35139	R. pipiens recombi
26	277.5	45.7	355	18	AAW35133	R. pipiens recombi
27	277.5	45.7	366	18	AAW35132	R. pipiens recombi
28	277.5	45.7	379	18	AAW35126	R. pipiens recombi
29	276.5	45.6	104	20	AAV28870	Recombinant RAPUR1
30	274.5	45.2	104	12	AAW12344	Protein with activ
31	274.5	45.2	104	15	AAW47303	ONCONASE (pharmac
32	274.5	45.2	104	17	AAW00736	Protein derived fr
33	274.5	45.2	104	18	AAW06543	Antitumour protein
34	274.5	45.2	104	18	AAW14065	Oncogene (RTM) pro
35	274.5	45.2	104	20	AAV33322	Frog onconase prot
36	274.5	45.2	104	20	AAW88233	Rana pipiens RNase
37	272.5	44.9	104	22	AAW31667	Amino acid sequenc
38	272.5	44.9	104	23	ABG31617	Northern leopard f
39	272.5	44.9	105	18	AAW35116	R. pipiens recombi
40	272.5	44.9	106	18	AAW35122	R. pipiens recombi
41	272.5	44.9	107	18	AAW35117	R. pipiens recombi
42	271.5	44.7	104	18	AAW30302	Recombinant onc pr
43	271.5	44.7	105	18	AAW35115	R. pipiens recombi
44	268.5	44.2	358	18	AAW35127	R. pipiens recombi
45	268.5	44.2	365	18	AAW35131	R. pipiens recombi

ALIGNMENTS

RESULT 1

AAV28873

ID AAV28873 standard; Protein; 111 AA.

XX

AC AAV28873;

XX

DT 25-JAN-2000 (first entry)

XX

DE Recombinant Met (-1) RaCOR1.

XX

Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;  
covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
RNase; autoimmune disease.

OS

OS Rana catesbeiana.

XX

XX Synthetic.

Key Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT

XX WO9950398-A2.

PN

XX Rana catesbeiana o

 XX | 07-OCT-1999. || XX |  | Recombinant Met (-1 |
XX		Recombinant RaCOR1
XX		Recombinant RaCOR1
XX		Frog lectin protei
XX		Recombinant Met (-1
XX		Antitumour protein

XX PI Newton DL, Rybak SM;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08131.  
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX PT treating cancers, viral infections or autoimmune diseases -  
 XX PS Claim 22; Page 63; 71pp; English.  
 XX CC The present sequence is a recombinant Rana catesbeiana oocyte  
 XX CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal  
 XX CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 XX CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 XX CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
 XX CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 XX CC N-terminal methionine due to the presence of a signal peptide that is  
 XX CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 XX CC proteins to be fused in-frame with ligand binding moieties to form  
 XX CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 XX CC autoimmune diseases.  
 XX SQ Sequence 111 AA;  
 Query Match 100.0%; Score 607; DB 20; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-62; Indels 0; Gaps 0;  
 Matches 111; Conservative 0; Mismatches 0;  
 QY 1 MQNWTFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNV 60  
 DB 1 MQNWTFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNV 60  
 QY 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 DB 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 RESULT 2  
 AAY28872  
 ID AAY28872 standard; Protein; 110 AA.  
 XX AC AAY28872;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.  
 XX KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;  
 XX KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma;  
 XX KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;  
 XX KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;  
 XX KW RNase.  
 XX OS Rana catesbeiana.  
 XX OS Synthetic.  
 XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US06641.  
 XX PR 27-MAR-1998; 98US-0079751.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Newton DL, Rybak SM;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08130.  
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -  
 XX PS Claim 22; Page 62; 71pp; English.  
 XX CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)  
 XX CC protein encoded by a cDNA modified for expression in E. coli. Carboxy  
 XX CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,  
 XX CC which can be a LL2 antibody directed against CD22 on cancerous B cells  
 XX CC or human chorionic gonadotrophin (hCG) effective against Kaposi's  
 XX CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria  
 XX CC without an N-terminal methionine due to the presence of a signal peptide  
 XX CC that is cleaved by bacteria. The soluble expression of ribonuclease  
 XX CC allows the proteins to be fused in-frame with ligand binding moieties to  
 XX CC form cytotoxic fusion proteins. They can be used for treatment of cancer  
 XX CC and autoimmune diseases.  
 XX SQ Sequence 110 AA;  
 Query Match 99.2%; Score 602; DB 20; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-61; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 0;  
 QY 2 QNWTFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNV 61  
 DB 1 QNWTFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNV 60  
 QY 62 STTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 DB 61 STTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 RESULT 3  
 AAY28878  
 ID AAY28878 standard; Protein; 111 AA.  
 XX AC AAY28878;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Recombinant Met (-1) RaCOR1 GlnSer amino acid sequence.  
 XX KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease GlnSer; RaCOR1;  
 XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 XX KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
 XX KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 XX KW CD22; RNase; autoimmune disease.  
 XX OS Rana catesbeiana.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"  
 XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US06641.  
 XX PR 27-MAR-1998; 98US-0079751.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Newton DL, Rybak SM;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08135.  
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX PT treating cancers, viral infections or autoimmune diseases -

XX PS Claim 22; Page 68; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana ribonuclease

CC (RaCOR1) protein with Met at position 1 and Gln28Ser. Carboxy terminal end

CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which

CC can be a LL2 antibody directed against CD22 on cancerous B cells or human

CC chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.

CC Recombinant ribonucleases can be expressed in bacteria without an N-

CC terminal methionine due to the presence of a signal peptide that is

CC cleaved by bacteria. The soluble expression of ribonuclease allows the

CC proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and

CC autoimmune diseases.

XX SQ Sequence 111 AA;

Query Match 99.2%; Score 602; DB 20; Length 111;

Best Local Similarity 99.1%; Pred. No. 2.7e-61;

Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

DB 1 MSNATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

DB 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

RESULT 4

AAV28876

ID AAY28876 standard; Protein; 111 AA.

XX AC AAY28876;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6 protein.

XX KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1;

XX KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;

XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;

XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

XX KW cancer; bullfrog; RNase; autoimmune disease.

XX OS Rana catesbeiana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 23 /note= "Wild type Met replaced with Leu"

FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

XX PN W09950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US06641.

XX PR 27-MAR-1998; 98US-0079751.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Newton DL, Rybak SM;

XX DR WPI: 1999-610847/52.

XX DR N-PSDB; AA208133.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -

XX PS Claim 22; Page 66; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana oocyte

CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a

CC (His)6 tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant

CC RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2

CC antibody directed against CD22 on cancerous B cells or human chorionic

CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases.

XX SQ Sequence 111 AA;

Query Match 99.0%; Score 601; DB 20; Length 111;

Best Local Similarity 98.2%; Pred. No. 3.5e-61;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

DB 1 MOWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

DB 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

RESULT 5

AAV28877

ID AAY28877 standard; Protein; 110 AA.

XX AC AAY28877;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant RaCOR1 Gln1Ser amino acid sequence.

XX KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;

XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;

XX KW bullfrog; Kaposi's sarcoma; human chorionic gonadotropin; hCG; RNase;

XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

XX KW cancer; autoimmune disease.

XX OS Rana catesbeiana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

XX PN W09950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US06641.

XX PR 27-MAR-1998; 98US-0079751.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Newton DL, Rybak SM;

XX DR WPI: 1999-610847/52.

XX DR N-PSDB; AA208134.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -  
XX Claim 22; Page 67; 71pp; English.  
XX The present sequence is a recombinant Rana catesbeiana oocyte  
CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of  
CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
CC can be a LL2 antibody directed against CD22 on cancerous B cells or  
CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
CC N-terminal methionine due to the presence of a signal peptide that is  
CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
CC proteins to be fused in-frame with ligand binding moieties to form  
CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
CC autoimmune diseases.  
XX Sequence 110 AA;  
SQ Query Match 98.4%; Score 597; DB 20; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1e-60;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 NWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 62  
Db 2 NWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 61  
Qy 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
RESULT 6  
AA28874  
ID AAY28874 standard; Protein; 110 AA.  
XX  
AC AAY28874;  
XX  
DT 25-JAN-2000 (first entry)  
XX  
DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.  
XX  
KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;  
KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;  
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;  
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
KW cancer; bullfrog; RNase; autoimmune disease.  
XX  
OS Rana catesbeiana.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 22 /note= "Wild type Met replaced with Leu"  
FT Misc-difference 57 /note= "Wild type Met replaced with Leu"  
FT  
PN WO9950398-A2.  
XX  
PD 07-OCT-1999.  
XX  
PF 26-MAR-1999; 99WO-US06641.  
XX  
PR 27-MAR-1998; 98US-0079751.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Newton DL, Rybak SM;  
XX  
DR WPI; 1999-610847/52.  
XX  
DR N-PSDB; AAZ08132.  
XX  
XX New recombinant ribonucleases, used for killing target cells, e.g. for  
PT treating cancers, viral infections or autoimmune diseases -

XX Claim 22; Page 64; 71pp; English.  
XX The present sequence is a recombinant Rana catesbeiana oocyte  
CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal  
CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
CC which can be a LL2 antibody directed against CD22 on cancerous B cells  
CC or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
CC N-terminal methionine due to the presence of a signal peptide that is  
CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
CC proteins to be fused in-frame with ligand binding moieties to form  
CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
CC autoimmune diseases.  
XX Sequence 110 AA;  
SQ Query Match 98.2%; Score 596; DB 20; Length 110;  
Best Local Similarity 98.2%; Pred. No. 1.3e-60;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 QNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61  
Db 1 QNWATFQKHIIINTPIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
Qy 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
RESULT 7  
AA33321  
ID AAY33321 standard; Protein; 111 AA.  
XX  
AC AAY33321;  
XX  
DT 29-NOV-1999 (first entry)  
XX  
DE Frog lectin protein fragment.  
XX  
KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;  
KW heavy chain; cell surface marker; treatment; tumor; viral infection;  
KW parasite infection; immune dysfunctional cell; autoimmune disease;  
KW contraceptive; cell separation; transplantation; bone marrow ablation;  
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.  
XX  
OS Rana catesbeiana.  
XX  
PN US5955073-A.  
XX  
PD 21-SEP-1999.  
XX  
PF 09-JUL-1997; 97US-0891848.  
XX  
PR 22-SEP-1993; 93US-0125462.  
PR 22-OCT-1991; 91US-0779195.  
PR 20-APR-1990; 90US-0510696.  
PR 04-FEB-1993; 93US-0014082.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;  
XX  
DR WPI; 1999-560488/47.  
XX  
XX Recombinantly fused pancreatic RNase-targeting proteins useful for  
PT treating tumors, infections, immune or autoimmune disorders and as a  
PT contraceptive -  
XX  
PS Example 3; Fig 19; 47pp; English.  
XX  
XX This invention describes a novel nucleic acid construct comprising  
CC sequences encoding functional pancreatic RNase and a second protein

(preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog (Rana catesbeiana) lectin used to describe the method of the invention.

XX Sequence 111 AA;  
SQ Query Match 97.0%; Score 588.5; DB 20; Length 111;  
Best Local Similarity 98.2%; Pred. No. 9.7e-60;  
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
Qy 2 QNWTATFOOKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60  
Db 1 ENWTATFOOKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60  
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111  
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

RESULT 8  
AAV28867  
ID AAY28867 standard; Protein; 105 AA.  
AC AAY28867;  
XX 25-JAN-2000 (first entry)  
DT Recombinant Met (-1) RaPLR1.  
DE Recombinant Met (-1) RaPLR1.  
XX Recombinant Met (-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;  
KW covalently bound; L22 antibody; ligand binding moiety; cancerous B cell;  
KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
KW autoimmune disease.  
XX Rana pipiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"  
FT  
XX WO9950398-A2.  
XX 07-OCT-1999.  
XX 26-MAR-1999; 99WO-US06641.  
XX 27-MAR-1998; 98US-0079751.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA Newton DL, Rybak SM;  
PI Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
XX WPI; 1999-610847/52.  
DR N-PSDB; AA208126.  
XX New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases -

XX Claim 34; Page 57; 71pp; English.  
PS The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a L22 antibody directed against CD22 on cancerous B cells or human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases.  
XX Sequence 105 AA;  
SQ Query Match 47.2%; Score 286.5; DB 20; Length 105;  
Best Local Similarity 50.0%; Pred. No. 4.4e-25;  
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
Qy 1 MQNWTATFOOKHIIINT-PIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58  
Db 1 MODWLTTFQKHLTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEVPAKICKGIIASK 56  
Qy 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110  
Db 57 NVLTSEFYISDC---NVTSPCKYKUKKSTNTFCVTCTENQAPVHFVGVGHC 105

RESULT 9  
AAW06544  
ID AAW06544 standard; protein; 104 AA.  
XX AAW06544;  
AC AAW06544;  
XX 22-AUG-1997 (first entry)  
DT Antitumour protein from Rana pipiens oocytes.  
DE Tumour; chemotherapy; radiotherapy; frog.  
KW Rana pipiens.  
XX WO9639428-A1.  
XX 12-DEC-1996.  
XX 03-JUN-1996; 96WO-US08304.  
XX 06-JUN-1995; 95US-0467955.  
XX (ALFA-) ALFACELL CORP.  
XX Ardel WJ;  
XX WPI; 1997-043063/04.  
XX Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy  
XX Claim 8; Page 28; 45pp; English.

XX The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens oocytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treatment of tumours.  
XX Sequence 104 AA;  
SQ

```

Query Match      46.9%; Score 284.5; DB 18; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

OY 2 ONWATFOOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 59
Db 1 EDMLTFQKGGVNTTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
OY 60 VLSSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 110
Db 57 VLTITSEFVLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVCRC 104

RESULT 10
ID AAY28869 standard; Protein; 105 AA.
XX AC AAY28869;
XX DT 25-JAN-2000 (first entry)
XX DE Recombinant Met (-1) RaPLR1 Met23Leu- (His)6 protein.
XX KW Recombinant Met (-1) Rana pipiens ribonuclease Met23Leu- (His)6; RaPLR1;
XX KW CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
XX KW cancer; frog; autoimmune disease.
XX OS Rana pipiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
FT Misc-difference 24 /note= "Wild type Met replaced with Leu"
XX PN WO9950398-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US06641.
XX PR 27-MAR-1999; 98US-0079751.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA Newton DL, Rybak SM;
XX PI WPI; 1999-610847/52.
XX DR N-PSDB; AA208127.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PT treating cancers, viral infections or autoimmune diseases -
XX PS Claim 4; Page 59; 71pp; English.
XX CC The present sequence is a recombinant Rana pipiens ribonuclease protein
XX CC (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
XX CC Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
XX CC binding moiety, which can be a LL2 antibody directed against CD22 on
XX CC cancerous B cells or human chorionic gonadotrophin (hCG) effective
XX CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be
XX CC expressed in bacteria without an N-terminal methionine due to the
XX CC presence of a signal peptide that is cleaved by bacteria. The soluble
XX CC expression of ribonuclease allows the proteins to be fused in-frame with
XX CC ligand binding moieties to form cytotoxic fusion proteins. They can be
XX CC used for treatment of cancer and autoimmune diseases.

SQ Sequence 105 AA;
Query Match      46.7%; Score 283.5; DB 20; Length 105;
Best Local Similarity 49.1%; Pred. No. 9.8e-25;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

OY 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 QDWLTFQKGGVNTTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
OY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 110
Db 57 NVLTITSEFVLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVCRC 105

RESULT 11
ID AAY39400 standard; Protein; 105 AA.
XX AC AAY39400;
XX DT 01-DEC-1999 (first entry)
XX DE Recombinant frog Onconase.
XX KW Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
XX OS Rana pipiens.
XX PN WO9946389-A1.
XX PD 16-SEP-1999.
XX PF 11-MAR-1999; 99WO-US04252.
XX PR 11-MAR-1998; 98US-0077557.
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Goldenberg DM, Hansen H, Leung S;
XX WPI; 1999-551416/46.
XX DR N-PSDB; AA219767.
XX PT A new recombinant Onconase used to treat, e.g. colon cancer -
XX PS Example 1; Fig 1; 42pp; English.
XX CC This sequence represents recombinant frog Onconase. Onconase has
XX CC ribonuclease and anti-tumour activity. The cDNA was produced via PCR
XX CC (using primers AA219768-219769) of two synthetic DNAs whose sequences
XX CC encoded most of the N-terminal or the C-terminal amino acids of mature
XX CC Onconase. The two PCR products generated encoded either the N-terminal
XX CC 54 amino acids (minus the initial methionine) or the C-terminal 51 amino
XX CC acids, and were ligated in frame at an NruI site. The cDNA was then
XX CC subcloned into a vector e.g., pBluescript, where the ATG initiation
XX CC codon was ligated to the cDNA. After expression in E. coli, the
XX CC recombinant protein was purified. The initial N-formyl methionine was
XX CC cleaved off and the now N-terminal glutamate residue cyclised to form an
XX CC N-terminal pyroglutamate. The pyroglutamate residue forms part of the
XX CC phosphate binding pocket of Onconase and is essential for both
XX CC ribonuclease and anti-tumour activity. Onconase is a 12 kD ribonuclease
XX CC which causes cell death as a result of potent inhibition of protein
XX CC synthesis by a mechanism involving inactivation of cellular RNA. It is
XX CC not inhibited by mammalian placental ribonuclease inhibitor. It is
XX CC explain its enhanced cytotoxicity relative to mammalian enzymes. It has
XX CC anti-tumour activity against a variety of solid tumours e.g. colon or
XX CC pancreatic cancers, and can be used alone or in combination with other
XX CC anti-cancer agents such as taxofen. When used as an anti-tumour agent,
XX CC Onconase can be conjugated to a marker which targets it to a specific
XX CC cell type.
XX SQ Sequence 105 AA;
```





Db 57 NVLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 14  
AAV28879  
ID AAV28879 standard; Protein; 127 AA.  
XX  
AC AAV28879;  
XX  
DT 25-JAN-2000 (first entry)  
XX  
DE Rana pipiens Clone 5a1b ribonuclease.  
XX  
KW Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;  
KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;  
KW Kaposi's Sarcoma; human chorionic gonadotrophin; HCG; cancer;  
KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;  
KW autoimmune disease.  
XX  
OS Rana pipiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Signal peptide  
FT /note= "Putative"  
FT Protein 24..127  
FT /label= Rana\_pipiens\_Clone\_5a1b\_ribonuclease  
XX  
FN WO9950398-A2.  
XX  
PD 07-OCT-1999.  
XX  
PF 26-MAR-1999; 99WO-US06641.  
XX  
PR 27-MAR-1998; 98US-0079751.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Newton DL, Rybak SM;  
XX  
DR WPI; 1999-610847/52.  
DR N-PSDB; AAZ08136.  
XX  
PT New recombinant ribonucleases, used for killing target cells, e.g. for  
PT treating cancers, viral infections or autoimmune diseases -  
XX  
PS Disclosure; Page 69; 71pp; English.  
XX  
CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).  
CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA  
CC library. It exhibits differences with Onconase (RTM) at amino acid  
CC residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a  
CC covalently bound ligand binding moiety, which can be a B22 antibody  
CC directed against CD22 on cancerous B cells or human chorionic  
CC gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant  
CC ribonucleases can be expressed in bacteria without an N-terminal  
CC methionine due to the presence of a signal peptide that is cleaved by  
CC bacteria. The soluble expression of ribonuclease allows the proteins to  
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
CC proteins. They can be used for treatment of cancer and autoimmune  
XX diseases.  
XX  
SQ Sequence 127 AA;  
Query Match 46.4%; Score 281.5; DB 20; Length 127;  
Best Local Similarity 49.5%; Pred. No. 2.1e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFTFISSATTVKAICTGVI-NMN 59  
Db 24 QDWLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIISK 79  
QY 60 VLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVPVHFAGIGRC 110

Db 80 VLITSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 15  
AAW35123  
ID AAW35123 standard; Protein; 105 AA.  
XX  
AC AAW35123;  
XX  
DT 20-APR-1998 (first entry)  
XX  
DE R. pipiens recombinant RNase protein [Met-(-1)]rOnc.  
XX  
KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;  
KW tumour cell growth; frog.  
XX  
OS Rana pipiens.  
XX  
FN WO9731116-A2.  
XX  
PD 28-AUG-1997.  
XX  
PF 19-FEB-1997; 97WO-US02588.  
XX  
PR 21-FEB-1996; 96US-0011800.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Boque L, Newton DL, Rybak SM, Wlodawer A;  
XX  
DR WPI; 1997-435168/40.  
DR N-PSDB; AAT94959.  
XX  
PT Ribonuclease molecules based on native Onconase - used for killing  
PT cells, particularly tumour cells  
XX  
PS Disclosure; Pages 65-66; 90pp; English.  
XX  
CC AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are  
CC modifications of the RNase Onconase (RTM) (nOnc). Such novel  
CC ribonuclease molecules are highly cytotoxic and can be used alone or to  
CC form chemical conjugates or to target recombinant immunofusions. They are  
CC used particularly for decreasing tumour cell growth. They can also be  
CC used for cell separation in vitro by selectively killing unwanted types  
CC of cells, e.g. in bone marrow prior to transplantation into a patient  
CC undergoing marrow ablation by radiation, or for killing leukaemia cells  
CC or T-cells that would cause graft versus host disease. The toxins can  
CC also be used to selectively kill unwanted cells in culture. The new  
CC ribonucleases have increased cytotoxic activity compared to nOnc and also  
CC lower immunogenicity in humans.  
XX  
SQ Sequence 105 AA;  
Query Match 46.0%; Score 279.5; DB 18; Length 105;  
Best Local Similarity 49.1%; Pred. No. 2.8e-24;  
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
QY 1 MQNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFTFISSATTVKAICTGVI-NM 58  
Db 1 MEDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIISK 56  
QY 59 NVLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVPVHFAGIGRC 110  
Db 57 NVLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 105

Search completed: January 22, 2004, 12:06:23  
Job time : 34.9213 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.59176 Seconds  
(without alignments)  
784.758 Million cell updates/sec

Title: US-09-622-613C-19

Perfect score: 600

Sequence: 1 QNWATPQOKHIINTPIICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585.5	97.6	111	1	RNPO_RANCA
2	451	75.2	111	1	LECS_RANJA
3	370	61.7	111	1	RNPL_RANCA
4	273.5	45.6	104	1	RN30_RANPI
5	154.5	25.8	145	1	ANG3_MOUSE
6	149.5	24.9	145	1	ANGR_MOUSE
7	136.5	22.8	145	1	ANGI_MOUSE
8	131.5	21.9	124	1	RNP_BALAC
9	129.5	21.6	124	1	RNP_FIG
10	129.5	21.6	167	1	RNBR_BOVIN
11	127.5	21.2	119	1	RNP_IGUITG
12	124.5	20.8	151	1	RNBR_CAPCA
13	123.5	20.6	123	1	ANG2_BOVIN
14	123.5	20.6	141	1	RNBR_GIRCA
15	123.5	20.6	151	1	RNBR_AXIPR
16	123	20.5	146	1	ANGI_MIOFA
17	123	20.5	146	1	ANGI_SAISC
18	120	20.0	146	1	ANGI_CERAE
19	120	20.0	147	1	ANGI_PONPY
20	119.5	19.9	143	1	RNBR_SHEEP
21	119	19.8	122	1	RNP_MACRU
22	118.5	19.8	123	1	ANGI_PIG
23	118.5	19.8	124	1	RNP_ANTAM
24	118	19.7	146	1	ANGI_AOTTR
25	117	19.5	146	1	ANGI_SAGOE
26	116.5	19.4	128	1	RNP_MVOCO
27	116.5	19.4	149	1	RNP_MOUSE
28	115	19.1	146	1	ANGI_MACRU
29	114.5	19.1	128	1	RNBR_CAVPO
30	114	19.0	148	1	ANGI_BOVIN
31	113.5	18.9	124	1	RNP_CAMDR
32	113.5	18.9	128	1	RNP_HORSE
33	113	18.8	147	1	ANGI_HUMAN

## ALIGNMENTS

### RESULT 1

ID	RNPO_RANCA	STANDARD;	PRT;	111 AA.
AC	P11916;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ribonuclease, oocytes (BC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
RX	MEDLINE=87299649; PubMed=3304421;			
RA	Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana			
RT	catesbeiana) eggs."			
RL	Biochemistry 26:2189-2194(1987).			
RN	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana			
RT	catesbeiana (bullfrog) oocytes."			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,			
RA	Takayanagi Y., Hakomori S., Titani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana			
RT	catesbeiana eggs."			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=98437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes			
RT	of Rana catesbeiana (bullfrog)."			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine			
CC	residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)			
CC	as substrates, and prefers the former. The S-lectins in frog eggs			
CC	may be involved in the fertilization and development of the frog			
CC	embryo. This lectin agglutinates various animal cells, including			
CC	normal lymphocytes, erythrocytes, and fibroblasts of animal and			
CC	human origin.			
CC	-1- SUBUNIT: Monomer.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR; A27121; A27121.			

34	113	18.8	147	1	ANGI_PANTR
35	112.5	18.8	128	1	RNP_PROGU
36	109.5	18.2	124	1	RNP_RANTA
37	109.5	18.2	146	1	ANGI_PAPHA
38	109.5	18.2	148	1	RNS4_MOUSE
39	109	18.2	125	1	ANGI_RABIT
40	108.5	18.1	124	1	RNP_CAPCA
41	108.5	18.1	124	1	RNP_GIRCA
42	108.5	18.1	130	1	RNP_CRILLO
43	107.5	17.9	124	1	RNP_BUBBU
44	107.5	17.9	148	1	RNP_PERLE
45	107.5	17.9	149	1	RNP_ACOCA

Q8wme8	pan troglod
P04059	proechimys
P00566	rangifer ta
Q8wne4	papio hamad
Q9jjh1	mus musculus
P31347	oryctolagus c
P00664	capreolus c
P00662	giraffa cam
P24717	cricetulus
P00657	bubalus bub
Q9wuv5	peromyscus
Q9wtts5	acomys cahi



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SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;
Query Match 61.7%; Score 370; DB 1; Length 111;
Best Local Similarity 64.9%; Pred. No. 2.2e-33;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;
Qy 1 QNWATFOOKHIIINTPII-CNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QNWAKFKKHIRSTSSIDCNDTKMDKAIYIVGGCKKERTFIISSEDNVKAICSGVSPDK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ELSTTSFKLNTCIRDSITPRPCPYHSPDNNKICVKCEKQVPHFVGIGKC 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 4
RN30_RANPI STANDARD; PRT; 104 AA.
AC P22069;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P-30 protein (EC 3.1.1.27.-) (Onconase).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=91093131; PubMed=1985896;
RA Ardel T. W., Mikulski S.M., Shogen K.;
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL J. Biol. Chem. 266:245-251(1991).
RN [2]
RN 3D-STRUCTURE MODELING.
RX MEDLINE=93066156; PubMed=1438177;
RA Mosimann S.C., Johns K.L., Ardel T. W., Mikulski S.M., Shogen K.,
RA James M.N.G.;
RT "Comparative molecular modeling and crystallization of P-30 protein:
RT a novel antitumor protein of Rana pipiens oocytes and early
RT embryos.";
RL Proteins 14:392-400(1992).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94166079; PubMed=8120892;
RA Mosimann S.C., Ardel T. W., James M.N.G.;
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT amphibian ribonuclease with anti-tumor activity.";
RL J. Mol. Biol. 236:1141-1153(1994).
CC -1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY
CC AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR
CC IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH
CC MOLECULAR WEIGHT RIBOSOMAL RNA.
CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PDB; IONC; 31-JAN-94.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA.1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10
FT ACT_SITE 31 31
FT ACT_SITE 97 97
FT DISULFID 19 68
FT DISULFID 30 75
FT DISULFID 48 90
FT DISULFID 87 104
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FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT STRAND 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;
Query Match 45.6%; Score 273.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 6.1e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
Qy 1 QNWATFOOKHIIINT-PIICNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QDWLTFOKKHITNTRDVCNINMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
|||||:|||||:|||||:|||||:|||||:|||||:
Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLNKSTNKFVCVCENQAPVHFVGVGSC 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 5
ANG3 MOUSE STANDARD; PRT; 145 AA.
AC P97802;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE (BF-5)
GN ANG3 OR ANGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97184476; PubMed=9032278;
RA Fu X., Kamps M.P.;
RT "B2a-Pbx1 induces aberrant expression of tissue-specific and
RT developmentally regulated genes when expressed in NIH 3T3
RT fibroblasts.";
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U72672; AAC05794.1; -.
CC HSSP; P10152; IAGI.
CC MGD; MGI:1201793; Angl.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
DR
```

```
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16696 MW; DE9D3BC92F1D682C CRC64;

Query Match 25.8%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 7e-10; 23; Indels 9; Gaps 4;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;

Oy 33 CKRVNTFIISATTVKAIC-----TGVINLVLTTRFQNLNCTRTSITPR-PCPYSSR 85
Db 63 CKRVNTFIHDTKNKIKALCGNGRPGV-NFRI-SNSRFQVTTCTHKGSRPRPCQYNAP 120

Oy 86 TETNYICVKCENQYVPHF 103
Db 121 KDFRYIVIAICEDGWPVHF 138

RESULT 6
ANGR_MOUSE
ID -ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RL protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC or send an email to license@isb-sib.ch).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC EMBL; U22519; AAA91367.1; -.
CC HSP; P03950; 1A4Y.
DR MGD; MGI:104984; Angrp.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT POTENTIAL.
```

```
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 24.9%; Score 149.5; DB 1; Length 145;
Best Local Similarity 44.2%; Pred. No. 2.5e-09;
Matches 34; Conservative 9; Mismatches 27; Indels 7; Gaps 3;

Oy 33 CKRVNTFIISATTVKAICGV-----INLVLTTRFQNLNCTRTSITPR-PCPYSSRT 86
Db 63 CKRVNTFIHDTKNKIKALCGKSGPYGNLRI-SKSRFQVTTCTHKGSRPRPCRYRASK 121

Oy 87 ETNYICVKCENQYVPHF 103
Db 122 GFRYIIIGCENGWPVHF 138
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## RESULT 7

```
ANGI_MOUSE
ID -ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RL angiogenins: discernment of functionally important residues and
RN regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL; U22516; AAA91366.1; -.
CC PIR; A35932; A35932.
CC HSP; P03950; 1A4Y.
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FT ACT SITE 41 41 BY SIMILARITY.  
 FT ACT SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;  
 Query Match 21.6%; Score 129.5; DB 1; Length 124;  
 Best Local Similarity 30.7%; Pred. No. 3.1e-07;  
 Matches 35; Conservative 20; Mismatches 42; Indels 17; Gaps 6;  
 QY 6 FQOKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGV-INLN 58  
 DB 8 FORQHMDDPSSSSNYCNLMMSRR-NMTQGRCKPNTFVHESLADVQAVCSQINVNCK 66  
 QY 59 VLSTTRFQNT-----CTRITITPRP-CPYSSRTETNYICVKEQ--YPVHF 103  
 DB 67 NGQTCYQSNSTWHITDCRQTGSSKYPNCAYKASQEQKHIIIVACEGNPPVPVHF 120  
 RESULT 10  
 RNR BOVIN  
 ID RNR BOVIN STANDARD; PRT; 167 AA.  
 AC P39873;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).  
 GN BRN.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92093604; PubMed=1754384;  
 RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,  
 RA Viola M., Palmieri M., Russo E., Furia A.;  
 RT "Molecular cloning of the gene encoding the bovine brain ribonuclease  
 and its expression in different regions of the brain."  
 RL Nucleic Acids Res. 19:6469-6474(1991).  
 RN [2]  
 RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.  
 RC TISSUE=Brain;  
 RX MEDLINE=89214015; PubMed=3243767;  
 RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,  
 RA Ohgi K., Irie M.;  
 RT "Primary structure of a ribonuclease from bovine brain."  
 RL J. Biochem. 104:939-945(1988).  
 RN [3]  
 RP SEQUENCE OF 27-167 FROM N.A.  
 RX MEDLINE=96139017; PubMed=8587129;  
 RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,  
 RA Vento M.T., Furia A.;  
 RT "Molecular evolution of genes encoding ribonucleases in ruminant  
 species."  
 RL J. Mol. Evol. 41:850-858(1995).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
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 CC -----  
 DR EMBL; X59767; CAA42439.1; -.  
 DR EMBL; S81744; AAB36138.1; -.  
 DR PIR; S20066; S20066.  
 DR HSSP; P00656; 2RNS.

GlycoSuiteDB; P39873; -.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rna5A; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 167 RIBONUCLEASE, BRAIN.  
 FT ACT\_SITE 38 38 BY SIMILARITY.  
 FT ACT\_SITE 67 67 BY SIMILARITY.  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT DISULFID 52 110 BY SIMILARITY.  
 FT DISULFID 66 121 BY SIMILARITY.  
 FT DISULFID 84 136 BY SIMILARITY.  
 FT DISULFID 91 98 BY SIMILARITY.  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 155 155 /FTID-CAR\_000005.  
 FT CARBOHYD 159 159 O-LINKED.  
 FT CARBOHYD 155 155 O-LINKED.  
 FT CONFLICT 155 155 T -> S (IN REF. 2).  
 SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;  
 Query Match 21.6%; Score 129.5; DB 1; Length 167;  
 Best Local Similarity 30.6%; Pred. No. 4.2e-07;  
 Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;  
 QY 4 ATFOOKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINL 57  
 DB 32 AKFRQHMDSGSSSSNPNYCNQMKRR-RMTHGRCKPNTFVHESLDDVKAICS---OK 87  
 QY 58 NVL-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHFA 104  
 DB 88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKIVTACEGNPPVPVHF 147  
 QY 105 G 105  
 DB 148 G 148  
 RESULT 11  
 RNP IGUG  
 ID RNP IGUG STANDARD; PRT; 119 AA.  
 AC P80287;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
 OS Iguana iguana (Common iguana).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylia; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
 OX NCBI\_TaxID=8517;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=94139745; PubMed=8307028;  
 RA Zhao W., Beintema J.J., Hofsteenge J.;  
 RT "The amino acid sequence of iguana (Iguana iguana) pancreatic  
 ribonuclease."  
 RL Eur. J. Biochem. 219:641-646(1994).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Pancreas.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PIR; S4111; S4111.  
 DR HSSP; P00656; 1LSQ.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rna5A; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase P; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 25 80 BY SIMILARITY.  
 FT DISULFID 39 91 BY SIMILARITY.  
 FT DISULFID 57 106 BY SIMILARITY.  
 FT ACT SITE 10 10 BY SIMILARITY.  
 FT ACT SITE 40 40 BY SIMILARITY.  
 FT ACT SITE 113 113 BY SIMILARITY.  
 SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;  
 Query Match 21.2%; Score 127.5; DB 1; Length 119;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-07;  
 Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;  
 Qy 1 QNWATFOQKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAIC-- 51  
 Db 1 QDMSFQNKHIDYETSASNNAYCDLMMQRR-NLNPCKCKTRNTFVHASPEIQQVCGS 59  
 Qy 52 --TGVINLNLSTTRFQNLNCTRTSIT-PRCPYSSRTETNYICVKCENQYVPHF 103  
 Db 60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPTGTRIRIACENQYVPHF 114  
 RESULT 12  
 ID -RNBR CAPCA STANDARD; PRT; 151 AA.  
 AC P79351;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Capreolus capreolus (Roe deer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
 OC Cervidae; Odocolleinae; Capreolus.  
 OC NCBI\_TaxID=9858;  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=98278842; PubMed=9611269;  
 RA Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,  
 RA Beukelman J.J.;  
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";  
 RL Gene 212:259-268(1998).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
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 CC -----  
 CC EMBL; Y11673; CAA72371.1; -;  
 DR HSP; P00656; 1SRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase P; 1.  
 DR PROSITE; PS00127; RNASE PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
 FT ACT SITE 41 41 BY SIMILARITY.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 65 72 BY SIMILARITY.  
 FT CARBOHYD 62 62 N-LINKED (GLCNAC...); (BY SIMILARITY).  
 FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).  
 FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).

SQ SEQUENCE 151 AA; 16971 MW; 392D0B6302F006A6 CRC64;  
 Query Match 20.8%; Score 124.5; DB 1; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 1.3e-06;  
 Matches 34; Conservative 18; Mismatches 44; Indels 23; Gaps 6;  
 Qy 4 ATFOQKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINL 57  
 Db 6 AKFRQHMDSGSSSSGNPNYCNQMKRR-RMTHGCKPNTFVHESLDNVKAVCS---OK 61  
 Qy 58 NVL-----STTRFQNLNCTRTSITPRP-CYSSRTETNYICVKCENQ-YVPHF 103  
 Db 62 NITCKNGQPCYQSNSTNMNITDCRTGSSKYPNCAYKTSOKYITVACEGDPYVPHF 120  
 RESULT 13  
 ID -ANG2 BOVIN STANDARD; PRT; 123 AA.  
 AC P80929;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin-2 (EC 3.1.27.-).  
 GN ANG2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN SEQUENCE.  
 RX TISSUE=Milk, and Serum;  
 RX MEDLINE=9740980; PubMed=9266695;  
 RA Strydom D.J., Bond M.D., Vallee B.L.;  
 RT "An angiogenic protein from bovine serum and milk -- purification and  
 RT primary structure of angiogenin-2.";  
 RL Eur. J. Biochem. 247:535-544(1997).  
 CC -!- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.  
 CC -!- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC HSP; P10152; IAGI.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam; PF00074; rnaaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase P; 1.  
 DR PROSITE; PS00127; RNASE PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;  
 KW Protein synthesis inhibitor; Glycoprotein;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT SITE 12 12 BY SIMILARITY.  
 FT ACT SITE 39 39 BY SIMILARITY.  
 FT ACT SITE 113 113 BY SIMILARITY.  
 FT DISULFID 25 80  
 FT DISULFID 38 91  
 FT DISULFID 56 106  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC...);  
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;  
 Query Match 20.6%; Score 123.5; DB 1; Length 123;  
 Best Local Similarity 29.6%; Pred. No. 1.4e-06;  
 Matches 32; Conservative 20; Mismatches 43; Indels 13; Gaps 5;  
 Qy 6 FQKHINTPI-----ICNTILDNNIYVGGCKRVNTFISSATTVKAIC---TGVINL 57  
 Db 8 FLRKHDPSTGHDDRYCNYTMERR--NMTRPCKDNTFTIHGNSDDIRAVCDNRNGEYR 65  
 Qy 58 NVLSTTR--FQNLNCTRTSITPR-PCPYSSRTETNYICVKCENQYVPH 102





Db 122 G 122

Search completed: January 22, 2004, 12:02:09  
Job time : 6.59176 secs



Qy	1	QNWATFOQKHINTP-IICNTILDNNIYVGGQCKRVNTFFIISATTVAICTGV-INLN	58
Db	1	QNWAFQEKHIPNTSINCNTIMDKSIYVGGQCKERTNTFFIISATTVAICSGASTNRN	60
Qy	59	VLSTTRFOLNTCTRTSITRPPCPYSSRTETNYICVKCNQYVHPAGIGRC	109
Db	61	VLSTTRFOLNTCIRSATAPRCPYNSRTETNYICVKCNRLPVPVHPAGIGRC	111
RESULT 3			
JX0085			
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog			
C:Species: Rana catesbeiana (bullfrog)			
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994			
C:Accession: JX0085			
J:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg			
J:Biochem. 106, 729-735, 1989			
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.			
A:Reference number: JX0085; MUID:90130374; PMID:2613682			
A:Accession: JX0085			
A:Molecule type: protein			
A:Residues: 1-111 <NIT>			
C:Superfamily: pancreatic ribonuclease			
C:Keywords: hydrolase; pyroglutamic acid			
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
F:10.35.104/Active site: His, Lys, His #status predicted			
F:19-72.34-82.52-97.94-111/Disulfide bonds: #status predicted			
Query Match 61.7%; Score 370; DB 2; Length 111;			
Best Local Similarity 64.9%; Pred. No. 1.1e-29;			
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;			
Qy	1	QNWATFOQKHINTPIL-ONTILDNNIYVGGQCKRVNTFFIISATTVAICTGVI-NLN	58
Db	1	QNWAFQEKHIRSTSIDCNTIMDKAIYVGGCKERTNTFFIISDNDVKAICSGVSPDRK	60
Qy	59	VLSTTRFOLNTCTRTSITRPPCPYSSRTETNYICVKCNQYVHPAGIGRC	109
Db	61	ELSTTSFKLNTCIRDSITRPPCPYHSPDNNKICVKCKQLPVPVHGKGC	111
RESULT 4			
A39035			
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)			
C:Species: Rana pipiens (northern leopard frog)			
C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993			
C:Accession: A39035			
R:Ardelet, W.; Mikulecki, S.M.; Shogen, K.			
J:Biochem. 266, 245-251, 1991			
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl			
A:Reference number: A39035; MUID:91093131; PMID:1985896			
A:Accession: A39035			
A:Status: preliminary			
A:Molecule type: protein			
A:Residues: 1-104 <ARD>			
C:Superfamily: pancreatic ribonuclease			
Query Match 45.1%; Score 270.5; DB 2; Length 104;			
Best Local Similarity 47.7%; Pred. No. 7.2e-20;			
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;			
Qy	1	QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFFIISATTVAICTGVI-NLN	58
Db	1	EDWLTFQKHINTRDVDCNDIMSTNLF----HCKDKNTFFYSRPEPVKAICKGIIASKN	56
Qy	59	VLSTTRFOLNTCTRTSITRPPCPYSSRTETNYICVKCNQYVHPAGIGRC	109
Db	57	VLTTSEFVLSDC---NVTSRPCKYKIKLSTNKFVCTCENQAPVHPVGVGSC	104
RESULT 5			
A35932			
angiogenin precursor - mouse			

N:Alternate names: angiogenesis factor			
N:Contains: ribonuclease (EC 3.1.27.-)			
C:Species: Mus musculus (house mouse)			
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999			
C:Accession: A35932			
R:Bond, M.D.; Vallee, B.L.			
Biochem. Biophys. Res. Commun. 171, 988-995, 1990			
A:Title: Isolation and sequencing of mouse angiogenin DNA.			
A:Reference number: A35932; MUID:91025023; PMID:2222458			
A:Accession: A35932			
A:Status: not compared with conceptual translation			
A:Molecule type: DNA			
A:Residues: 1-145 <BON>			
A:Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:9726326			
C:Genetics:			
A:Introns: #status absent			
C:Function:			
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues			
C:Superfamily: pancreatic ribonuclease			
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid			
F:1-24/Domain: signal sequence #status predicted <SIG>			
F:25-145/Product: angiogenin #status predicted <MAT>			
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted			
F:37.64.137/Active site: His, Lys, His #status predicted			
F:50-104,63-115,81-130/Disulfide bonds: #status predicted			
Query Match 22.8%; Score 136.5; DB 1; Length 145;			
Best Local Similarity 40.3%; Pred. No. 1.8e-06;			
Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;			
Qy	33	CKRVNTFFIISATTVAICTG-----VINLVLTTRFOLNTCTRTSITPR-PCPYSSRT	86
Db	63	CKDVNTFFIHNKSNIKKICANGANGSPYRENL-RMSKPFQVTTCKTGTSRPPRCQVRAS	121
Qy	87	ETNYICVKCNQYVPVHF	103
Db	122	GFRHWIACENGLPVHF	138
RESULT 6			
NRWHK			
pancreatic ribonuclease (EC 3.1.27.5) - minke whale			
N:Alternate names: RNase 1; RNase A			
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)			
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994			
C:Accession: A00818			
R:Emmense, M.; Welling, G.W.; Beintema, J.J.			
Biochem. J. 157, 317-323, 1976			
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.			
A:Reference number: A00818; MUID:76277855; PMID:962870			
A:Accession: A00818			
A:Molecule type: protein			
A:Residues: 1-124 <EMM>			
C:Superfamily: pancreatic ribonuclease			
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas			
F:12.41.119/Active site: His, Lys, His #status predicted			
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted			
F:76/Binding site: carbohydrate (Aen) (covalent) (partial) #status experimental			
Query Match 21.9%; Score 131.5; DB 1; Length 124;			
Best Local Similarity 32.5%; Pred. No. 4.9e-06;			
Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;			
Qy	6	FQKHII-----NTPPICNTILDNNIYVGGQCKRVNTFFIISATTVAICTGVINLV	59
Db	8	FQKHII-----NTPPICNTILDNNIYVGGQCKRVNTFFIISATTVAICTGVINLV	59
Qy	60	L-----STTRFOLNTCTRTSITPR-CPYSSRTETNYICVKE-NOY-PVHF	103
Db	64	LCKNGRTNICYESNTMHTDCRQTGSSKYPNCAVTKQEKHIIVACSGNPVVPVHF	120
RESULT 7			

NRPG

pancreatic ribonuclease (EC 3.1.27.5) - pig  
N:Alternate names: RNase 1; RNase A  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C:Accession: A92071; A91391; A00816  
R:Jackson, R.L.; Hirs, C.H.W.  
J. Biol. Chem. 245, 637-653, 1970  
A:Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se  
A:Reference number: A92071; MUID:70104197; PMID:5460946  
A:Accession: A92071  
A:Molecule type: protein  
A:Residues: 1-'Q', 3-124 <JAC>  
R:Wierenga, R.K.; Huizinga, J.D.; Gaastera, W.; Welling, G.W.; Beintema, J.J.  
FEBS Lett. 31, 181-185, 1973  
A:Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation  
A:Reference number: A91391  
A:Accession: A91391  
A:Molecule type: protein  
A:Residues: 1-124 <WIE>  
R:Phelan, J.J.; Hirs, C.H.W.  
J. Biol. Chem. 245, 654-661, 1970  
A:Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo  
A:Reference number: A92072; MUID:70104198; PMID:4904878  
A:Contents: annotation: disulfide bonds  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:26-84,40-95,58-110,65-72/disulfide bonds: #status experimental

Query Match 21.6%; Score 129.5; DB 1; Length 124;  
Best Local Similarity 30.7%; Pred. No. 7.7e-06;  
Matches 35; Conservative 20; Mismatches 42; Indels 17; Gaps 6;

Qy 6 FQKH-----INTPLICNTILDNNIYVGGCKRVNTFIISATTVKAICTGV-INLN 58  
Db 8 FQKH-----INTPLICNTILDNNIYVGGCKRVNTFIISATTVKAICTGV-INLN 58  
Qy 59 VLSTRTQLNT-----CTRTSTPRP-CPVSSRTETNYICVCKENQ--YPVHF 103  
Db 67 NGQTCYQSNSTWHITDCRTGTGSSKYPNCAYKASOEKHIIVACEGNPPVPVHF 120

RESULT 8  
S20066  
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 22-Jun-1999  
C:Accession: S20066; JX0056  
R:Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri  
Nucleic Acids Res. 19, 6469-6474, 1991  
A:Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex  
A:Reference number: S20066; MUID:92093604; PMID:1754384  
A:Accession: S20066  
A:Molecule type: DNA  
A:Residues: 1-167 <SAS>  
R:Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sando, A.; Takizawa, Y.; Ohgi, K.; Iri  
J. Biochem. 104, 939-945, 1988  
A:Title: Primary structure of a ribonuclease from bovine brain.  
A:Reference number: JX0056; MUID:89214015; PMID:3243767  
A:Accession: JX0056  
A:Molecule type: protein  
A:Residues: 27-154, 'S', 156-166 <WAT>  
A:Experimental source: brain  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase  
F:38,67,145/Active site: His, Lys, His #status predicted  
F:52-110,66-121,84-136,91-98/disulfide bonds: #status predicted  
F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Db 7 FQRQHMDTEHSTASSSNYNLMMKAR-DWTSGRCKPLNTFIHEPKSVVDVACHQENVTCK 65

Qy 52 TGVINLNLVSTTRFQNLCTRTTSITPRP-CPYSSRTETNYICVKENQY-PVHF 103

Db 66 NGRNTNC-YKSNRSLITNCRQTGASKYPNCQVETSNLKNKQIIVACEGQYVPVHF 118

RESULT 11

A43825

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S29834; A43825

R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.

Biochim. Biophys. Acta 1162, 177-186, 1993

A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme

A:Reference number: S29833; MUID:93192291; PMID:8446182

A:Accession: S29834

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-123 <BON>

A:Note: this sequence was submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

Query Match 19.8%; Score 118.5; DB 1; Length 123;

Best Local Similarity 39.5%; Pred. No. 9.3e-05;

Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

Qy 33 CKRVNTFTFISSATTVKAICTG-----VINLNLVSTTRFQNLCTRTTSITPR-PCPYSSRTE 87

Db 39 CKEVNTFTGTRNDIKAICNDKNGEPYNNFRSRKSPFQITTCCHKKGSSNRPPCGVRATAG 98

Qy 88 TNYICVKENQYVPVHF 103

Db 99 FRTIIVACENGLPVHF 114

RESULT 12

NRPRI

pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Antilocapra americana (pronghorn)

C:Date: 28-Feb-1981 #sequence\_revision 28-Feb-1981 #text\_change 31-Mar-2000

C:Accession: A00813

R:Beintema, J.J.; Gaastera, W.; Munniksma, J.

J. Mol. Evol. 13, 305-316, 1979

A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw

A:Reference number: A00813; MUID:80075014; PMID:513141

A:Accession: A00813

A:Molecule type: protein

A:Residues: 1-124 <BEI>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41,119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 19.8%; Score 118.5; DB 1; Length 124;

Best Local Similarity 29.9%; Pred. No. 9.4e-05;

Matches 35; Conservative 19; Mismatches 44; Indels 19; Gaps 7;

Qy 4 ATFOQKHINTPI-----ICNTILDNNIYVGGQCKRVNTFTFISSATTVKAICT----- 52

Db 6 AKFERQHIDSNFSSVSSSNYNQNMKSR-NLTQGRCKPVNTFVHESLADVQAVCSQKNVA 64

Qy 53 ---GVINLNLVSTTRFQNLCTRTTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103

Db 65 CKNGQTC-NQYSYMSITDCRETGSSKYPNCAYKTQAKHIIIVACEGPNPVPVHY 120

RESULT 13

NRU

pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Myocastor coypus (nutria, coypu)

C:Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000

C:Accession: A00822

R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.

Biochim. Biophys. Acta 453, 400-409, 1976

A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic ;

A:Reference number: A06612; MUID:77065676; PMID:999896

A:Accession: A00822

A:Molecule type: protein

A:Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41,119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.4%; Score 116.5; DB 1; Length 128;

Best Local Similarity 30.8%; Pred. No. 0.00015;

Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

Qy 6 FQQKHI-----INTPICNTILDNNIYVGGQCKRVNTFTFISSATTVKAICTGVINLNV 59

Db 8 FERQHMDSRGSPSTNPNYCNEMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy 60 L-----STTRFQNLCTRTTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103

Db 64 LCKNGQTCYOSNSNMHITDCRVTSNDSYFSCSYRSTOEEKSIIVACEGPNPVPVHF 120

RESULT 14

NRMS

pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse

N:Alternate names: RNase 1; RNase A

C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999

C:Accession: A34090; S22598; A00830

R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.

Mol. Biol. Evol. 7, 29-44, 1990

A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse

A:Reference number: A34090; MUID:90136034; PMID:2299980

A:Accession: A34090

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-149 <SCH>

A:Cross-references: GB:M27814; MID:g200762; PIDN:AAA40060.1; PID:g200763

R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.

Nucleic Acids Res. 19, 6935-6941, 1991

A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific

A:Reference number: S22598; MUID:92107684; PMID:1840677

A:Accession: S22598

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-149 <SAM>

A:Cross-references: EMBL:X60103; MID:g53981; PIDN:CAA42697.1; PID:g53982

R:Lenstra, J.A.; Beintema, J.J.

Eur. J. Biochem. 98, 399-408, 1979

A:Title: The amino acid sequence of mouse pancreatic ribonuclease.

A:Reference number: A00830; MUID:80024269; PMID:556267

A:Accession: A00830

A:Molecule type: protein

A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-149/Product: pancreatic ribonuclease #status experimental <SIG>

F:37.66,114/Active site: His, Lys, His #status predicted

F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted

F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 116.5; DB 1; Length 149;

Best Local Similarity 29.9%; Pred. No. 0.00018;

Matches 35; Conservative 17; Mismatches 42; Indels 23; Gaps 7;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 26.161 Seconds  
(without alignments)  
869.271 Million cell updates/sec

Title: US-09-622-613C-19

Perfect score: 600

Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGICRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	100.0	110	11	US-09-961-400-19
2	600	100.0	111	11	US-09-948-391A-21
3	600	100.0	111	11	US-09-961-400-21
4	600	100.0	117	11	US-09-948-391A-22
5	600	100.0	117	11	US-09-961-400-22
6	596	99.3	110	11	US-09-948-391A-15
7	596	99.3	110	11	US-09-961-400-15
8	596	99.3	111	11	US-09-961-400-17
9	594	99.0	110	11	US-09-948-391A-19
10	591	98.5	110	11	US-09-948-391A-24
11	591	98.5	110	11	US-09-961-400-24
12	591	98.5	111	11	US-09-948-391A-26
13	591	98.5	111	11	US-09-961-400-26
14	590	98.3	111	11	US-09-948-391A-17
15	279.5	46.6	111	11	US-09-961-400-9

16	277.5	46.2	104	11	US-09-961-400-2	Sequence 2, Appli
17	277.5	46.2	105	11	US-09-948-391A-6	Sequence 6, Appli
18	277.5	46.2	105	11	US-09-961-400-6	Sequence 6, Appli
19	277.5	46.2	127	11	US-09-948-391A-28	Sequence 28, Appli
20	277.5	46.2	127	11	US-09-961-400-28	Sequence 28, Appli
21	276.5	46.1	104	11	US-09-948-391A-2	Sequence 2, Appli
22	276.5	46.1	104	11	US-09-948-391A-4	Sequence 4, Appli
23	276.5	46.1	104	11	US-09-961-400-4	Sequence 4, Appli
24	276.5	46.1	105	11	US-09-961-400-8	Sequence 8, Appli
25	273.5	45.6	105	15	US-10-153-882-2	Sequence 2, Appli
26	272.5	45.4	104	11	US-09-948-391A-11	Sequence 11, Appli
27	272.5	45.4	104	11	US-09-961-400-11	Sequence 11, Appli
28	272.5	45.4	105	11	US-09-948-391A-13	Sequence 13, Appli
29	272.5	45.4	105	11	US-09-961-400-13	Sequence 13, Appli
30	268.5	44.8	104	10	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.8	104	11	US-09-918-887-1	Sequence 1, Appli
32	267.5	44.6	105	11	US-09-948-391A-8	Sequence 8, Appli
33	267.5	44.6	111	11	US-09-948-391A-9	Sequence 9, Appli
34	202	33.7	83	10	US-09-986-119-3	Sequence 3, Appli
35	202	33.7	83	11	US-09-918-887-3	Sequence 3, Appli
36	161	26.8	169	13	US-10-016-447-2	Sequence 2, Appli
37	127.5	21.2	119	12	US-10-074-978A-139	Sequence 139, App
38	118	19.7	99	12	US-10-074-978A-141	Sequence 141, App
39	117	19.5	147	10	US-09-731-872-254	Sequence 254, App
40	117	19.5	147	12	US-09-876-997-254	Sequence 254, App
41	114	19.0	124	13	US-10-016-447-5	Sequence 5, Appli
42	113	18.8	147	9	US-09-286-240-6	Sequence 6, Appli
43	113	18.8	147	9	US-09-863-777-2	Sequence 2, Appli
44	110.5	18.4	124	10	US-09-981-286A-8	Sequence 8, Appli
45	110	18.3	131	13	US-10-016-447-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-961-400-19  
; Sequence 19, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961.400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-19

Query Match	100.0%	Score	600;	DB	11;	Length	110;
Best Local Similarity	100.0%	Pred. No.	2.9e-60;				
Matches	110;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFTIISATTVAICTGVINLNVL	60				
Db	1	QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFTIISATTVAICTGVINLNVL	60				
Qy	61	STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGICRCP	110				
Db	61	STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGICRCP	110				



```
RESULT 2
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met (-1) RaCOR1 Met22Leu Met57Leu)
US-09-948-391A-21

Query Match      100.0%; Score 600; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.9e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60
Db 2 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 61

Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 111

RESULT 3
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
```

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US-09-961-400-21

Query Match      100.0%; Score 600; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.9e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60
Db 2 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 61

Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 111

RESULT 4
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6)
US-09-948-391A-22

Query Match      100.0%; Score 600; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60
Db 8 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 67

Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 68 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 117

RESULT 5
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
```

```

; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match      100.0%; Score 600; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 67

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 68 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 6
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match      99.3%; Score 596; DB 11; Length 110;
Best Local Similarity 98.2%; Pred. No. 8.1e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 60

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match      99.3%; Score 596; DB 11; Length 110;
Best Local Similarity 98.2%; Pred. No. 8.1e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 60

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 8
US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match      99.3%; Score 596; DB 11; Length 111;
Best Local Similarity 98.2%; Pred. No. 8.2e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 60
```

Db 2 QNWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 61

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
|||||

RESULT 9

US-09-948-391A-19

; Sequence 19, Application US/09948391A

; Publication No. US20030027311A1

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: The United States of America

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Recombinant Anti-Tumor RNase

; FILE REFERENCE: 015280-343110US

; CURRENT APPLICATION NUMBER: US/09/948,391A

; CURRENT FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: US 60/079,751

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: WO PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: US 09/622,613

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Rana

; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and

; OTHER INFORMATION: Met57Leu substitutions (recombinant RacOR1

; OTHER INFORMATION: Met22Leu Met57Leu)

US-09-948-391A-19

Query Match 99.0%; Score 594; DB 11; Length 110;

Best Local Similarity 99.1%; Pred. No. 1.4e-59;

Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 60  
|||||

Db 1 QNWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 60  
|||||

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

RESULT 10

US-09-948-391A-24

; Sequence 24, Application US/09948391A

; Publication No. US20030027311A1

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: The United States of America

; APPLICANT: as represented by The Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Recombinant Anti-Tumor RNase

; FILE REFERENCE: 015280-343110US

; CURRENT APPLICATION NUMBER: US/09/948,391A

; CURRENT FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: US 60/079,751

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: WO PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: US 09/622,613

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Rana

; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution

; OTHER INFORMATION: (recombinant RacOR1 Q1S)

US-09-948-391A-24

Query Match 98.5%; Score 591; DB 11; Length 110;

Best Local Similarity 98.2%; Pred. No. 3e-59;

Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 61  
|||||

Db 2 NWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 61  
|||||

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

RESULT 11

US-09-961-400-24

; Sequence 24, Application US/09961400

; Publication No. US20030124131A1

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: GOLDENBERG, DAVID M.

; APPLICANT: NEWTON, DIANNE L.

; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

; FILE REFERENCE: 018733/1059

; CURRENT APPLICATION NUMBER: US/09/961,400

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: 09/622,613

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/079,751

; PRIOR FILING DATE: 1998-03-26

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Rana catesbeiana

US-09-961-400-24

Query Match 98.5%; Score 591; DB 11; Length 110;

Best Local Similarity 98.2%; Pred. No. 3e-59;

Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 61  
|||||

Db 2 NWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVNL 61  
|||||

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
|||||

RESULT 12

US-09-948-391A-26

; Sequence 26, Application US/09948391A

; Publication No. US20030027311A1

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: The United States of America

; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbelana ribonuclease with Met at position 1  
; OTHER INFORMATION: and GlnSer substitution (Met(-1) RacOR1 Q1S)  
US-09-948-391A-26

Query Match 98.5%; Score 591; DB 11; Length 111;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 NWATFOQKHIIPTIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 61  
Db 3 NWATFOQKHIIPTIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 62  
  
Qy 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 63 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 13  
US-09-961-400-26  
; Sequence 26, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbelana  
US-09-961-400-26

Query Match 98.5%; Score 591; DB 11; Length 111;  
Best Local Similarity 98.2%; Pred. No. 3e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 NWATFOQKHIIPTIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 61  
Db 3 NWATFOQKHIIPTIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 62  
  
Qy 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Db 63 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 14  
US-09-948-391A-17  
; Sequence 17, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbelana ribonuclease with Met at position 1  
; OTHER INFORMATION: (recombinant Met(-1) RacOR1)  
US-09-948-391A-17

Query Match 98.3%; Score 590; DB 11; Length 111;  
Best Local Similarity 97.3%; Pred. No. 3.9e-59;  
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 QNWATFOQKHIIPTIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINLNVL 60  
Db 2 QNWATFOQKHIIPTIICNTILDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61  
  
Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 15  
US-09-961-400-9  
; Sequence 9, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 111  
; TYPE: PRT



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:30 : Search time 13.1835 Seconds  
(without alignments)  
353.031 Million cell updates/sec

Title: US-09-622-613C-19  
Perfect score: 600  
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYVHFAGRCRP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	97.1	111	2	US-08-891-848-12
2	582.5	97.1	111	3	US-08-875-811-8
3	280.5	46.8	104	1	US-08-467-955-2
4	273.5	45.6	104	3	US-09-394-268-1
5	273.5	45.6	104	3	US-09-394-268-2
6	273.5	45.6	104	4	US-09-687-748-1
7	273.5	45.6	104	4	US-09-687-748-2
8	273.5	45.6	129	3	US-08-875-811-63
9	273.5	45.6	379	3	US-08-875-811-43
10	270.5	45.1	104	1	US-08-283-971-1
11	270.5	45.1	104	1	US-07-921-619-1
12	270.5	45.1	104	1	US-08-467-955-1
13	270.5	45.1	104	2	US-08-891-848-13
14	270.5	45.1	105	3	US-08-875-811-39
15	270.5	45.1	355	3	US-08-875-811-41
16	270.5	45.1	358	3	US-08-875-811-51
17	268.5	44.8	104	3	US-08-875-811-1
18	268.5	44.8	104	4	US-09-071-672-1
19	268.5	44.8	106	3	US-08-875-811-28
20	268.5	44.8	107	3	US-08-875-811-30
21	268.5	44.8	112	3	US-08-875-811-32
22	268.5	44.8	251	3	US-08-875-811-59
23	268.5	44.8	254	3	US-08-875-811-61
24	268.5	44.8	355	3	US-08-875-811-49
25	268.5	44.8	355	3	US-08-875-811-57
26	268.5	44.8	355	3	US-08-875-811-64
27	268.5	44.8	366	3	US-08-875-811-55

28	263.5	43.9	105	3	US-08-875-811-24	Sequence 24, Appl
29	263.5	43.9	105	3	US-08-875-811-26	Sequence 26, Appl
30	259.5	43.2	358	3	US-08-875-811-45	Sequence 45, Appl
31	259.5	43.2	365	3	US-08-875-811-53	Sequence 53, Appl
32	245.5	40.9	107	3	US-08-875-811-20	Sequence 20, Appl
33	235.5	39.2	111	3	US-08-875-811-22	Sequence 22, Appl
34	232	38.7	114	3	US-09-223-118-3	Sequence 3, Appl
35	223.5	37.2	360	3	US-08-875-811-47	Sequence 47, Appl
36	223	37.2	114	3	US-09-223-118-2	Sequence 2, Appl
37	222	37.0	114	3	US-09-223-118-1	Sequence 1, Appl
38	221	36.8	114	3	US-09-223-118-4	Sequence 4, Appl
39	202	33.7	83	3	US-08-875-811-2	Sequence 2, Appl
40	202	33.7	83	4	US-09-071-672-3	Sequence 3, Appl
41	161	26.8	169	1	US-08-441-629-2	Sequence 2, Appl
42	161	26.8	169	3	US-08-776-207-2	Sequence 2, Appl
43	161	26.8	169	4	US-09-507-773-2	Sequence 2, Appl
44	161	26.8	169	5	PCT-US95-09172-2	Sequence 2, Appl
45	123.5	20.6	125	6	5171845-2	Patent No. 5171845

ALIGNMENTS

RESULT 1  
US-08-891-848-12  
; Sequence 12, Application US/08891848  
; Patent No. 5955073  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Youle, Richard J.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Nicholls, Peter J.  
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,848  
; FILING DATE: No. 5955073 yet assigned  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,462  
; FILING DATE: 22-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/014,082  
; FILING DATE: 04-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/779,195  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/510,696  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-110110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-891-848-12

Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 4.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOOKHIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 59
Db 1 ENWATFOOKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMV 60

QY 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045791
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111

; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-875-811-8

Query Match 97.1%; Score 582.5; DB 3; Length 111;
Best Local Similarity 96.4%; Pred. No. 4.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOOKHIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 59
Db 1 ENWATFOOKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMV 60

QY 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
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APPLICATION NUMBER: US 07/436,141  
 FILING DATE: 13-NOV-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/814,332  
 FILING DATE: 03-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/283,970  
 FILING DATE: 01-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jay, Mark H.  
 REGISTRATION NUMBER: 27507  
 REFERENCE/DOCKET NUMBER: 5007 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-912-9066  
 TELEFAX: 201-912-0442  
 TELEX: No. 572805 Applicable  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: N  
 ANTI-SENSE: N  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: Rana pipiens  
 DEVELOPMENTAL STAGE: Oocyte  
 US-08-467-955-1

Query Match 45.1%; Score 270.5; DB 1; Length 104;  
 Best Local Similarity 47.7%; Pred. No. 5.2e-24;  
 Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 QNWATFOQRHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58  
 Db 1 EDMLTFQKHINTTRDVCNDIMSTNLF---HCKDKNTFIYSRPPVKAICKGIIASKN 56  
 QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 Db 57 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 13  
 US-08-891-848-13  
 Sequence 13, Application US/08891848  
 Patent No. 5955073  
 GENERAL INFORMATION:  
 APPLICANT: Rybak, Susanna M.  
 APPLICANT: Youle, Richard J.  
 APPLICANT: Newton, Dianne L.  
 APPLICANT: Nicholls, Peter J.  
 TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/891,848  
 FILING DATE: No. 5955073 yet assigned  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/125,462

FILING DATE: 22-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/014,082  
 FILING DATE: 04-FEB-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/779,195  
 FILING DATE: 22-OCT-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/510,696  
 FILING DATE: 20-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Ellen Lauver  
 REGISTRATION NUMBER: 32,762  
 REFERENCE/DOCKET NUMBER: 015280-110310US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..104  
 OTHER INFORMATION: /label= Onc  
 OTHER INFORMATION: /note= "Oncanase from Rana pipiens"  
 US-08-891-848-13

Query Match 45.1%; Score 270.5; DB 2; Length 104;  
 Best Local Similarity 47.7%; Pred. No. 5.2e-24;  
 Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 QNWATFOQRHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58  
 Db 1 EDMLTFQKHINTTRDVCNDIMSTNLF---HCKDKNTFIYSRPPVKAICKGIIASKN 56  
 QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 Db 57 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 14  
 US-08-875-811-39  
 Sequence 39, Application US/08875811  
 Patent No. 6045793  
 GENERAL INFORMATION:  
 APPLICANT: Rybak, Susanna M.  
 APPLICANT: Newton, Dianne L.  
 APPLICANT: Boque, Lluís  
 APPLICANT: Wlodawer, Alexander  
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
 NUMBER OF SEQUENCES: 64  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/875,811  
 FILING DATE: 19-FEB-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US97/02588

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;
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-39

Query Match 45.1%; Score 270.5; DB 3; Length 105;
Best Local Similarity 47.7%; Pred. No. 5.3e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVAICTGVI-NLN 58
Db 2 EDMLTFQKKHITNTRDVCNDIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
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RESULT 15
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-41

Query Match 45.1%; Score 270.5; DB 3; Length 355;
Best Local Similarity 47.7%; Pred. No. 2.3e-23;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

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Db 252 EDMLTFQKKHITNTRDVCNDIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 307

Qy 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
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Job time : 13.1835 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 34.6067 Seconds  
(without alignments)  
504.524 Million cell updates/sec

Title: US-09-622-613C-19

Perfect score: 600

Sequence: 1 QNWATFQKHIIINTPIICNT.....ICVKENQYVHPFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesecq\_19Jun03.\*  
1: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1980.DAT.\*  
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11: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1990.DAT.\*  
12: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1991.DAT.\*  
13: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1992.DAT.\*  
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16: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1995.DAT.\*  
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18: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1997.DAT.\*  
19: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1998.DAT.\*  
20: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA1999.DAT.\*  
21: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA2000.DAT.\*  
22: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA2001.DAT.\*  
23: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA2002.DAT.\*  
24: /SIDSI1/gcgdata/genesecq/genesecp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	100.0	110	20	AAV28874
2	600	100.0	111	20	AAV28876
3	586	99.3	110	20	AAV28872
4	586	99.3	111	20	AAV28877
5	591	98.5	110	20	AAV28873
6	591	98.5	111	20	AAV28878
7	582.5	97.1	111	20	AAV33321
8	280.5	46.8	104	18	AAW06544
9	279.5	46.6	104	20	AAV28866

10	279.5	46.6	105	20	AAV28869	Recombinant Met(-1
11	277.5	46.2	104	20	AAV28865	Rana pipiens liver
12	277.5	46.2	105	20	AAV28867	Recombinant Met(-1
13	277.5	46.2	127	20	AAV28879	Rana pipiens Clone
14	273.5	45.6	104	18	AAW30301	Recombinant onc pr
15	273.5	45.6	104	22	AAW31666	Amino acid sequenc
16	273.5	45.6	104	22	AAW31667	Amino acid sequenc
17	273.5	45.6	104	23	ABG31617	Northern leopard f
18	273.5	45.6	104	23	ABG32650	Northern leopard f
19	273.5	45.6	105	20	AAV39400	Recombinant frog O
20	273.5	45.6	379	18	AAW35126	R. pipiens recombi
21	272.5	45.4	104	18	AAW30302	Recombinant onc pr
22	272.5	45.4	104	20	AAV28870	Recombinant RapLRI
23	272.5	45.4	105	20	AAV28871	Recombinant Met(-1
24	270.5	45.1	104	12	AAW12344	Protein with activ
25	270.5	45.1	104	15	AAW47303	ONCONASE (pharmace
26	270.5	45.1	104	17	AAW00736	Protein derived fr
27	270.5	45.1	104	18	AAW06543	Antitumour protein
28	270.5	45.1	104	18	AAW14065	Onconase (RTM) pro
29	270.5	45.1	104	20	AAV33322	Onconase (RTM) pro
30	270.5	45.1	104	20	AAW88233	Frog onconase prot
31	270.5	45.1	105	18	AAW35123	R. pipiens RNase
32	270.5	45.1	355	18	AAW35125	R. pipiens recombi
33	270.5	45.1	358	18	AAW35130	R. pipiens recombi
34	268.5	44.8	106	18	AAW35122	R. pipiens recombi
35	268.5	44.8	107	18	AAW35117	R. pipiens recombi
36	268.5	44.8	112	18	AAW35118	R. pipiens recombi
37	268.5	44.8	251	18	AAW35134	R. pipiens recombi
38	268.5	44.8	254	18	AAW35135	R. pipiens recombi
39	268.5	44.8	355	18	AAW35129	R. pipiens recombi
40	268.5	44.8	355	18	AAW35133	R. pipiens recombi
41	268.5	44.8	366	18	AAW35132	R. pipiens recombi
42	263.5	43.9	104	18	AAW18224	Antitumour generi
43	263.5	43.9	105	18	AAW35115	R. pipiens recombi
44	263.5	43.9	105	18	AAW35116	R. pipiens recombi
45	259.5	43.2	358	18	AAW35127	R. pipiens recombi

## ALIGNMENTS

RESULT 1  
AAV28874  
ID AAY28874 standard; Protein; 110 AA.

AC AAY28874;  
XX  
XX 25-JAN-2000 (first entry)

Recombinant RacOR1 Met22Leu Met57Leu amino acid sequence.

Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;  
RacOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;  
cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;  
signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
cancer; bullfrog; RNase; autoimmune disease.

OS Rana catesbeiana.  
XX Synthetic.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 22 /note= "Wild type Met replaced with Leu"  
FT Misc-difference 57 /note= "Wild type Met replaced with Leu"

FT

XX

PN W09950398-A2.

XX

PD 07-OCT-1999.

XX

PF 26-MAR-1999; 99WO-US06641.

XX

PR 27-MAR-1998; 98US-0079751.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Newton DL, Rybak SM;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08132.  
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX PT treating cancers, viral infections or autoimmune diseases -  
 XX PS Claim 22; Page 64; 71pp; English.  
 XX CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells  
 CC or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases.  
 XX SQ Sequence 110 AA;  
 Query Match 100.0%; Score 600; DB 20; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-60;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
 DB 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
 QY 61 STTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 DB 61 STTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 RESULT 2  
 AAY28876  
 ID AAY28876 standard; Protein; 111 AA.  
 XX AC AAY28876;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6 protein.  
 XX KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1;  
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; bullfrog; RNase; autoimmune disease.  
 XX OS Rana catesbeiana.  
 XX OS Synthetic.  
 PH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"  
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"  
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"  
 XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.

PP 26-MAR-1999; 99WO-US06641.  
 XX PR 27-MAR-1998; 98US-0079751.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Newton DL, Rybak SM;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08133.  
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX PT treating cancers, viral infections or autoimmune diseases -  
 XX PS Claim 22; Page 66; 71pp; English.  
 XX CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a  
 CC (His)6 tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant  
 CC RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2  
 CC antibody directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases.  
 XX SQ Sequence 111 AA;  
 Query Match 100.0%; Score 600; DB 20; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-60;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
 DB 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 61  
 QY 61 STTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 DB 62 STTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 RESULT 3  
 AAY28872  
 ID AAY28872 standard; Protein; 110 AA.  
 XX AC AAY28872;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.  
 XX KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;  
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;  
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;  
 KW RNase.  
 XX OS Rana catesbeiana.  
 XX OS Synthetic.  
 XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US06641.  
 XX PR 27-MAR-1998; 98US-0079751.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Newton DL, Rybak SM;  
 XX WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08130.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases -  
 XX  
 PS Claim 22; Page 62; 71pp; English.  
 XX  
 CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)  
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy  
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells  
 CC or human chorionic gonadotropin (hCG) effective against Kaposi's  
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria  
 CC without an N-terminal methionine due to the presence of a signal peptide  
 CC that is cleaved by bacteria. The soluble expression of ribonuclease  
 CC allows the proteins to be fused in-frame with ligand binding moieties to  
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer  
 CC and autoimmune diseases.  
 XX  
 SQ Sequence 110 AA;  
 Query Match 99.3%; Score 596; DB 20; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.7e-59;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
 DB 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 RESULT 4  
 AAY28873  
 ID AAY28873 standard; Protein; 111 AA.  
 XX  
 AC AAY28873;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant Met (-1) RaCOR1.  
 XX  
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 KW RNase; autoimmune disease.  
 XX  
 OS Rana catesbeiana.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 FT  
 XX  
 PN WO9950398-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US06641.  
 XX  
 PR 27-MAR-1998; 98US-0079751.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Newton DL, Rybak SM;  
 XX WPI; 1999-610847/52.  
 DR  
 XX

DR N-PSDB; AAZ08131.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases -  
 XX  
 PS Claim 22; Page 63; 71pp; English.  
 XX  
 CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases.  
 XX  
 SQ Sequence 111 AA;  
 Query Match 99.3%; Score 596; DB 20; Length 111;  
 Best Local Similarity 98.2%; Pred. No. 1.8e-59;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60  
 DB 2 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 61  
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 DB 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 RESULT 5  
 AAY28877  
 ID AAY28877 standard; Protein; 110 AA.  
 XX  
 AC AAY28877;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant RaCOR1 Gln1Ser amino acid sequence.  
 XX  
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotropin; hCG; RNase;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; autoimmune disease.  
 XX  
 OS Rana catesbeiana.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"  
 FT  
 XX  
 PN WO9950398-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US06641.  
 XX  
 PR 27-MAR-1998; 98US-0079751.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Newton DL, Rybak SM;  
 XX WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08134.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -  
XX  
PS Claim 22; Page 67; 71pp; English.  
XX  
CC The present sequence is a recombinant Rana catesbeiana oocyte  
CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of  
CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
CC can be a L12 antibody directed against CD22 on cancerous B cells or  
CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma  
CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
CC N-terminal methionine due to the presence of a signal peptide that is  
CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
CC protein to be fused in-frame with ligand binding moieties to form  
CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
CC autoimmune diseases.  
XX  
SQ Sequence 110 AA;  
Query Match 98.5%; Score 591; DB 20; Length 110;  
Best Local Similarity 98.2%; Pred. No. 6.4e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 61  
Db 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 61  
Oy 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
RESULT 6  
AAV28878  
ID AAV28878 standard; Protein; 111 AA.  
XX  
AC AAV28878;  
XX  
DT 25-JAN-2000 (first entry)  
XX  
DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.  
XX  
KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;  
KW covalently bound; L12 antibody; ligand binding moiety; cancerous B cell;  
KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
KW CD22; RNase; autoimmune disease.  
XX  
OS Rana catesbeiana.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1  
FT Misc-difference 2 /note= "Met not found in wild type RaCOR1"  
FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"  
XX  
XX WO950398-A2.  
XX  
XX 07-OCT-1999.  
XX  
XX 26-MAR-1999; 99WO-US06641.  
XX  
XX 27-MAR-1998; 98US-0079751.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Newton DL, Rybak SM;  
XX  
XX WPI; 1999-610847/52.  
XX  
XX N-PSDB; AAZ08135.  
XX  
XX New recombinant ribonucleases, used for killing target cells, e.g. for  
XX treating cancers, viral infections or autoimmune diseases -  
PT

XX Claim 22; Page 68; 71pp; English.  
XX  
CC The present sequence is a recombinant Rana catesbeiana ribonuclease  
CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end  
CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
CC can be a L12 antibody directed against CD22 on cancerous B cells or human  
CC chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.  
CC Recombinant ribonucleases can be expressed in bacteria without an N-  
CC terminal methionine due to the presence of a signal peptide that is  
CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
CC protein to be fused in-frame with ligand binding moieties to form  
CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
CC autoimmune diseases.  
XX  
SQ Sequence 111 AA;  
Query Match 98.5%; Score 591; DB 20; Length 111;  
Best Local Similarity 98.2%; Pred. No. 6.5e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 61  
Db 3 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 62  
Oy 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 63 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
RESULT 7  
AAV33321  
ID AAV33321 standard; Protein; 111 AA.  
XX  
AC AAV33321;  
XX  
DT 29-NOV-1999 (first entry)  
XX  
DE Frog lectin protein fragment.  
XX  
KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;  
KW heavy chain; cell surface marker; treatment; tumor; viral infection;  
KW parasite infection; immune dysfunctional cell; autoimmune disease;  
KW contraceptive; cell separation; transplantation; bone marrow ablation;  
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.  
XX  
OS Rana catesbeiana.  
XX  
XX US5955073-A.  
XX  
XX 21-SEP-1999.  
XX  
XX 09-JUL-1997; 97US-0891849.  
XX  
XX 22-SEP-1993; 93US-0125462.  
XX  
XX 22-OCT-1991; 91US-0779195.  
XX  
XX 20-APR-1990; 90US-0510696.  
XX  
XX 04-FEB-1993; 93US-0014082.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Rybak SM, Newton DL, Nicholls PJ, Youle RJ;  
XX  
XX WPI; 1999-560488/47.  
XX  
XX Recombinantly fused pancreatic RNase-targeting proteins useful for  
XX treating tumors, infections, immune or autoimmune disorders and as a  
XX contraceptive -  
XX  
XX Example 3; Fig 19; 47pp; English.  
XX  
XX This invention describes a novel nucleic acid construct comprising  
XX sequences encoding functional pancreatic RNase and a second protein  
XX



(preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog (Rana catesbeiana) lectin used to describe the method of the invention.

Query Match 97.1%; Score 582.5; DB 20; Length 111;  
Best Local Similarity 96.4%; Pred. No. 5.9e-58;  
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOOKHIIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59  
Db 1 ENWATFOOKHIIINTPIINCNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60  
Qy 60 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110  
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8  
AAW06544  
ID AAW06544 standard; protein; 104 AA.

AC AAW06544;  
XX 22-AUG-1997 (first entry)  
XX Antitumour protein from Rana pipiens oocytes.  
XX Tumour; chemotherapy; radiotherapy; frog.

OS Rana pipiens.  
XX WO9639428-A1.  
XX 12-DEC-1996.  
XX 03-JUN-1996; 96WO-US08304.  
XX 06-JUN-1995; 95US-0467955.  
XX (ALFA-) ALFACELL CORP.  
XX Ardel WJ;  
XX WPI; 1997-043063/04.

XX Antitumour proteins from Rana pipiens oocyte(s) - have fewer  
XX disadvantages than chemotherapy, surgery and radiotherapy  
XX Claim 8; Page 28; 45pp; English.

XX The present sequence is a specifically claimed example of an  
XX antitumour protein from the generic protein in AAW18224, with the  
XX molecular weight 12000. This is one of two preferred proteins (the  
XX other in AAW06543) that have been isolated from Rana pipiens oocytes.  
XX Both proteins have a blocked amino terminal group and are essentially  
XX free of carbohydrates. The proteins are used to treat tumours. Use of  
XX the peptides has fewer disadvantages than chemotherapy, radiotherapy

CC and surgery in the treatment of tumours.

XX SQ Sequence 104 AA;

Query Match 46.8%; Score 280.5; DB 18; Length 104;  
Best Local Similarity 48.6%; Pred. No. 6.8e-24;  
Matches 54; Conservative 17; Mismatches 31; Indels 9; Gaps 4;

Qy 1 QNWATFOOKHIIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 58  
Db 1 EDWLTFOKKHVTNTRDVCNNIMSTNLF----HCKDKQNTFIYSRPEPVKAICKGIIASKN 56  
Qy 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 109  
Db 57 VLTTFSEFVLSDC---NVTSRCKYKLLKSTNKFVCVCENQAPVHFVGVGRC 104

RESULT 9  
AAW28866  
ID AAY28866 standard; protein; 104 AA.

AC AAY28866;  
XX 25-JAN-2000 (first entry)  
XX Recombinant RapLR1 Met23Leu amino acid sequence.

XX Recombinant Rana pipiens ribonuclease; RapLR1 Met23Leu; covalently bound;  
XX LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;  
XX Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
XX autoimmune disease.

OS Rana pipiens.  
OS Synthetic.

XX Key Location/Qualifiers  
XX Misc-difference 23 /note= "Wild type Met replaced with Leu"  
XX WO9950398-A2.

XX 07-OCT-1999.  
XX 26-MAR-1999; 99WO-US06641.  
XX 27-MAR-1998; 98US-0079751.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;  
XX WPI; 1999-610847/52.  
XX N-PSDB; AAZ08125.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
XX treating cancers, viral infections or autoimmune diseases -

XX Claim 34; Page 56; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLR1)  
XX protein with Met23Leu. Carboxy terminal end of recombinant RapLR1 has a  
XX covalently bound ligand binding moiety, which can be a LL2 antibody  
XX directed against CD22 on cancerous B cells or human chorionic  
XX gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
XX ribonucleases can be expressed in bacteria without an N-terminal  
XX methionine due to the presence of a signal peptide that is cleaved by  
XX bacteria. The soluble expression of ribonuclease allows the proteins to  
XX be fused in-frame with ligand binding moieties to form cytotoxic fusion  
XX proteins. They can be used for treatment of cancer and autoimmune  
XX diseases.

XX SQ Sequence 104 AA;





Db 80 VLTTFEYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 14  
AAW30301  
ID AAW30301 standard; protein; 104 AA.  
XX  
AC AAW30301;  
XX  
DT 09-JUN-1998 (first entry)  
XX  
DE Recombinant onc protein.  
XX  
KW Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer;  
KW human immunodeficiency virus type-1; HIV1; replication.  
XX  
OS Rana pipiens.  
XX  
PN WO9738112-A1.  
XX  
PD 16-OCT-1997.  
XX  
PF 04-APR-1997; 97WO-US05675.  
XX  
PR 04-APR-1996; 96US-0626288.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Ardelit W, Boix E, Vasandani VM, Wu YN, Youle RJ;  
XX  
DR WPI; 1997-512725/47.  
XX  
PT Recombinant Onc protein with glutamine residue at position 1 -  
PT useful as antitumour and antiviral agent, also as cell culture  
PT selection agent  
XX  
PS Claim 1; Page 28; 35pp; English.  
XX  
CC This sequence represents a recombinant Onc protein comprising a 104 amino  
CC acid sequence having Gln at position 1. Onc, a ribonuclease from Rana  
CC pipiens oocytes, is known as an antitumour agent (e.g. for treating  
CC pancreatic cancer) and inhibitor of human immunodeficiency virus type-1  
CC replication. It can be used therapeutically or as a cell-culture  
CC selection agent, e.g. to identify gene therapy compositions able to  
CC inhibit tumour growth.  
XX  
SQ Sequence 104 AA;  
Query Match 45.6%; Score 273.5; DB 18; Length 104;  
Best Local Similarity 48.6%; Pred. No. 4.2e-23;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVI-NLN 58  
DB 1 QDWLTFQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIATSKN 56  
QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109  
DB 57 VLTTFEYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 15  
AAB31666  
ID AAB31666 standard; protein; 104 AA.  
XX  
AC AAB31666;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a frog ribonuclease protein.  
XX  
KW Frog; ribonuclease; ranpirnase; RNase.

OS Rana pipiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "this Gln is autocyclised to pyroglutamic acid"  
XX  
PN US6175003-B1.  
XX  
PD 16-JAN-2001.  
XX  
PF 10-SEP-1999; 99US-0394268.  
XX  
PR 10-SEP-1999; 99US-0394268.  
XX  
PA (ALFA-) ALFACELL CORP.  
XX  
PI Saxena SK;  
XX  
DR WPI; 2001-167808/17.  
XX  
PT New nucleic acids encoding a ribonuclease (Rnase), useful for the  
PT precise targeting of Rnase to a predetermined cell receptor -  
XX  
PS Claim 1; Columns 5-6; 7pp; English.  
XX  
CC The present sequence represents a frog ribonuclease protein (ranpirnase)  
CC (Rnase). The specification describes a synthetic ribonuclease protein,  
CC in which the addition of cysteine in the ribonuclease facilitates the  
CC chemical linking of a targeting molecule by the single reactive  
CC sulphydryl group. The specification also describes a method for the  
CC production of ranpirnase using DNA technology instead of processing  
CC biological material. The re-engineering of the protein molecule allows  
CC easier attachment to a targeting molecule thereby making it possible for  
CC the ribonuclease to be delivered to a particular cell receptor where it  
CC might be most effective.  
XX  
SQ Sequence 104 AA;  
Query Match 45.6%; Score 273.5; DB 22; Length 104;  
Best Local Similarity 48.6%; Pred. No. 4.2e-23;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVI-NLN 58  
DB 1 QDWLTFQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIATSKN 56  
QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109  
DB 57 VLTTFEYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

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Job time : 35.6067 secs